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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 12, 2003, 11:07:32; Search time 21 Seconds (without alignments) 62.459 Million cell updates/sec Run on:

US-09-446-543A-5 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

328717 Total number of hits satisfying chosen parameters:

328717 seqs, 42310358 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq Length: 200000000

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 45 summaries

Database :

Issued Patents AA:

1. /cgf2 / fptodata1/iaa/5A_COMB.pep:*

2. /cgn2 / fptodata1/iaa/5B_COMB.pep:*

3. /cgn2 / fptodata1/iaa/6A_COMB.pep:*

4. /cgn2 / fptodata1/iaa/6B_COMB.pep:*

5. /cgn2 / fptodata1/iaa/PCTUS_COMB_pep:*

6. /cgn2 / fptodata1/iaa/PCTUS_COMB_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query	Leng-h	DB	GI	Description	
 rd 	172	100.0			-105-	Sequence 7 Appli	
2	172	100.0	31	m	US-09-105-678A-31	Seguence 31, Appl	
m	172	200.0	31	m	-77	'n	
4	172	190.0	31	m	JS-08-776-971-97	97,	
m	172	100.0	31	m	-09-421-	7.	
0 ا	172	100.0	11	m	US-09-421-208-31	31,	
7	172	100.0	31	4	95-60-	13,	
œ	172	100.0	32	m	-09	Sequence 32, Appl	
6	172	100.0	32	M	-80-	ø	
10	172	100.0	32	m	-421-	Sequence 32, Appl	
11	172	100.0	33	m	US-09-105-678A-33	2	
12	172	100.0	33	m	9	,	
ĒΞ	172	100.0		m	0	33	
7	172	100.0		m	9	ť	
15	172	100.0		m	-08-	Seguence 44, Appl	
9 4	172	100.0	98	m	-08	12	
5	172	100.0	96	m	-98-	131,	
18	172	100.0	96	m	-08-	136,	
61	168	7.76	96	m	-08-776-	115,	
20	168		86	m	-08	117.	
21	163		31	m	ö	9, A	
22	163		31	ŀΥ	US-09-105-678A-37	37	
23	163	94.8	31	L)	ě	4.	
	163		31	(L)	-08	Sequence 47, Appl	
25	163	٠.	31	m	US-09-421-208-8	æ	
	163	94.8	31	m	-09-421-20	37	
27	163	94.8	31	4	US-09-560-915-14	Sequence 14, Appl	

Sequence 4, Appli Sequence 38, Appl Sequence 38, Appl Sequence 39, Appl Sequence 39, Appl Sequence 45, Appl Sequence 45, Appl Sequence 124, Appl Sequence 29, Appl Sequence 29, Appli Sequence 29, Appli Sequence 3, Appli Sequence 61, Appli			
955.4 678A-38 678A-38 208.148 678A-39 971.46 971.47 971.124 971.13 971.13 678A-29 678A-29 678A-3 678A-3 678A-3	ALIGNMENTS BA PRODUCING A 19F2 LIGAND ROBERTS & CUSHMAN, LLP	. Version #2.30 78A 997	34.5
1 US-09-09-09-09-09-09-09-09-09-09-09-09-09-	910567 Sp of DD OF FEIN,	-DOS #1.0 05.6	- 994
99499999999999999999999999999999999999	a contraction	COUNTRY: WOSECON STATE: WOSA COUNTRY: USA COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE SOFTWARE: PREENT PREEDS/MS- SOFTWARE: PREEDT PREEDS/MS- SOFTWARE: PREEDT PREEDS/MS- SOFTWARE: PREEDT NUMBER: US/09/10 FILING DATE: 26-UTM-1998 PRIOR APPLICATION NUMBER: US/09/10 FILING DATE: 26-UTM-1998 TILING DATE: 27-UTM-1998 TILING DATE: 27-UTM-1997 NAME: CONLIN, DANIG G.	RESISTRATION NOWERS: 27,026 REFERENCE/DOCKET NUMBER: 49 TELECOMMUNICATION INFORMATION: TELEPRAX: 617-523-3400 TELEPRAX: 617-523-6440 FORRATION FOR SEQ 1D NO: 7. SEQUENCE CHARACTERISTICS: LENGTH: 31 amino acids TYPE: amino acid TYPE: amino acid TYPE: 1near TYPE: 1near TYPE: 1near
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	1 105-678 ence 7, nt No. PPLICAN PPLICAN PPLICAN PPLICAN OWBER ORRESPC ORRESPC	STATE: MS CONTRY: BOSCON STATE: MS COUNTRY: USA COUNTRY: USA COMPUTER READABLE F MEDIUM TYPE: FLO COMPUTER: IBM PC OPERATION SOFTWARE: SOFTWARE: SOFTWARE: SOFTWARE: LAND COURTING DATE: 27-ATTORNEY/AGENT INFO NAME: CONTIN, DA	RESERVETION REFERENCE/DO TELECOMMUNICAT TELEPHONE: TELEPAX: INFORMATION FOR. SEQUENCE CHARA LENGTH: 31 LENGTH: 31 LYPE: amino STRANDEDNESS TYDE: amino STRANDEDNESS TOPLOGY: 1
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Query Match
100.0%; Score 172; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 31; Conservative 0; Mismatches 0; Indels

, MOLECULE TYPE: peptide US-09-105-678A-7

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Gaps ö

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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hinuma, Shuji
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MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                               Boston
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US-08-776-971-97
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
10C.0%: Score 172; DB 3; Length 31;
Best Local Similarity 10C.0%: Pred. No. 1.3e-19;
Matches 31; Conservative 0: Mismatches 0; Indels
                                                                                                                                                                                           APPLICANT: Suenaga. Masalo
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Mishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-UN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,0026
REGISTRATION NUMBER: 27,0026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 48166-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                               Sequence 31, Application US/09105678A Patent No. 6103882 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-08-776-971-5
Sequence 5, Application US/08776971B
FPERT NO. 6228684
GENERAL INFORMATION:
Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide US-09-105-678A-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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STREET: 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        02109
                                                                                    RESULT 2
US-09-105-678A-31
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TITLE OF INVENTION. Chieko
NUMBER OF SEQUENCE: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 31; Conservative 0; Mismatches 0, Indels
COMPTR: . USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IED mompacible
OCNEDIUM SYSTEM: DOS
OFTWARE: PactSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,9718
FILING DATE: 06-Feb-1997
CLASSIFICATION NUMBER: PCT/1P96/0382:
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 9/
FILING DATE: 12-NG-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-NG-1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 12-AGG-1996
APPLICATION NUMBER: JP 8/21805
APPLICATION
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MOLECULE TYPE: peptide
                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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COMPUTER READABLE FORM:

MEDIUW TYPE: Diskette
COMPUTER: ISM comparible
COMPUTER: CASCIFICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION NUMBER: UP 7/44371
APPLICATION NUMBER: UP 7/43371
APPLICATION NUMBER: UP 8/59419
FILING DATE: 18-DEC-1996
APPLICATION NUMBER: UP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: UP 8/59419
FILING DATE: 15-A0419
FILING DATE: 12-A041996
APPLICATION NUMBER: UP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: UP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: 27.026
REGISTRATION NUMBER: 27.026
REGISTRATION NUMBER: 27.026
REFERRANE/DOCKET NUMBER: 27.026
REGISTRATION NUMBER: 27.026
REFERRANE/DOCKET NUMBER: 27.026
REGISTRATION NUMBER: 27.026
REFERRANE/DOCKET NUMBER: 27.026
REFERRANE/D
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APPLICANT: Moriya, Takeo
APPLICANT: Araka, Yoko
APPLICANT: Taraka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5: DIKE, BRONSTEIN. ROBERTS & CUSHMAN. LLP
130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compactible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421.208
FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%: Score 172; DB 3:
Best Local Similarity 160.0%; Pred. No. 1.3e-19;
Matches 31; Conservative 0: Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDENESS: single
SPOUCOY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 97:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09421208
Patent No. -6258561
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDALL
STREET: Loc
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US-09-421-208-7
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5 P

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Query Match 100.0%; Score 172; DB 3; Length 31; Best Local Similarity 100.0%; Pred. No. 1.3e-19; Matches 31; Conservative 0; Mismatches 0; Indels
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APPLICANT: Moriya, Takeo
APPLICANT: Mariya, Takeo
APPLICANT: Mashimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19PZ LIGAND
CORRESPONDENCES: $2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E. DIKE, BRONSTEIN, ROBERTS & CUSHMAN. LLP
130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #I.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGRF 31
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MEDIUM TYRE: Floopy disk
COMPUTER: 1BM C Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PATOMIN Release #1.0. Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421, 208
FILING DATE: PATOMIN DATA:
APPLICATION NUMBER: US 09/105, 678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
ATTORNEY/AGENT INFORMATION:
                  FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JF 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
US 09/105,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 31, Application US/09421208
Patent No. 6258561
GENERAL INFORMATION:
                                                                                                                      NAME: Collin, David G.
REGISTRATION NUMBER: 27,026
REPERENCE/DOCKET NUMBER: 4846(
TELECORMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
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REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4846
FELECOMMINICATION INFORMATION:
TELEPHONE: 617-523-3400
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
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LENGTH: 32 amino acids
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US-08-776-971-6
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                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                  APPELICANT: Civelli, Olivier
APPLICANT: Civelli, Olivier
APPLICANT: Lin. Steven
TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRF)
FILE REFERENCE: P-UC 3534
CURRENT APPLICATION NUMBER: US/139/560.915
CURRENT FILING DATE: 2:00-04-28
NUMBER OF 5E0 ID NCS: 24
SOCTWARE: FastSEQ for Windows Version 4.0
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100.0%; Score 172; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 31: Conservative 0; Mismatches 0; Indels
                                                            Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 32, Application US/0910567BA
Fatent No. 6103B82
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Anaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CONTY: Boston
                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ITAM PC. COMPATIBLE
COMPUTER: THAN PC. COMPATIBLE
OPERATIOG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT ARPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                              100.0%; Score 172; DB 3;
100.0%; Pred. No. 1.3e-19;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                                                        US-09-560-915-13
Sequence 13 Application US/09560915
Patent NO 6387764
GENERAL INFORMATION:
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                                      Ouery Match
Best Local Similarity luv.
Best Local 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conlin, David G.
; MOLECULE TYPE: peptide
US-09-421-208-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 13
LENGTH: 31
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Gaps
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Kitada, Chieko
TITLE OF INVENTON: POLYPROTEINS, THEIR FRCDUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESSED ADDRESSES:
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                   Length 32:
                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

COMPUTER: IBM compatible

CORRUTER: IBM compatible

CORRUTER: TBM COMPATA;

SOFTWARE: FastSEO for Windows Version 2.0

CURRENT APPLICATION NUMBER: US/08/776,971B

FILING DATE: 06-66-1997

CLASSIFICATION NUMBER: PCT/fp96/03821

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: DT/fy96/03821

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: DP/f33371

FILING DATE: 12-AUG-1996

APPLICATION NUMBER: DP/f34371

FILING DATE: 12-AUG-1996

APPLICATION NUMBER: DP/F311B05

FILING DATE: 12-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: COALIN, DAVIG 6

REFERENCE/DOCKET NUMBER: 27, D26

REFERENCE/DOCKET NUMBER: 27, D26

REFERENCE/DOCKET NUMBER: 27, D26
                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 172; DB 3; Best Local Similarity 100.0%: Pred. No. 1.3e-19; Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                             1 SRAHOHSMEIRTPOINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                      1 SRAHQHSNEIRTPDINPAWYAGRGIRPVGRF 3.
    48466-342
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Patent No. 6228984
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
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REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-640
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hinuma, Shuji
                                                                                                                                      LENGTH: 32 amino acids TYPE: amino acid
                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
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RESULT 1
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                                                                                                                                                                     100.0%; Score 172; DB 3; Length 32; 100.0%; Pred. No. 1.3e-19; tive 0; Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
ITILE OF INSTITUTE OF INSTITUTE OF INSTITUTE OF INSTITUTE OF INSTITUTE OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5: DIKE, BRONSTEIN, ROBERTS & CUSHMAN. LLP
130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02109

ZIP: 02109

MEDIUM TYPER READABLE FORM:
MEDIUM TYPEP Floppy disk
COMPUTER: IDM PC compatible
OPERATING SYSTEW: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0. Version #1.3C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421.208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                                          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 17218/1997
FILING DATE: 27-JUN-1997
ATTOMEY/AGENT INFORMATION:
NAME: COLLIE, DAVIG G.
REGISTRATION NUMBER: 27,026
REFERENCE/POCKET NUMBER: 48466-342
TELEPHONE:
FILEPHONE: 617-523-340
                 STRANDEDNESS: single
TOPCLOGY: linear
MOLECULE TYPE: procein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 6,
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 32, Application US/09421208
Patent No. 6258561
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEC ID NO: 32:
SECJENCE CHARACTERISTICS:
LENGIH: 32 amino acids
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Best Local Similarity 100.0°
Matches 31; Conservative
                                                                                                                                                                                                               31: Conservative
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-421-208-32
                                                                                                                                                                       Query Match
Best Local Similarity
Matches 31: Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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STATE: M
COUNTRY:
                                                                                                                             US-08-776-971-6
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C: Gaps
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TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, JLP
ATREET: 130 Water Street
CITY: BOSCON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 172; DB 3; Length 33: Best Local Similarity 100.0%; Pred. No. 1.4e-19; Matches 31; Conservative 0; Mismatches 0: Inde:s
                                                                                             APPLICANT: Suenaga, Masatc
APPLICANT: Moriya. Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SRAHQHSMEIRTPDINPAWYAGRGİRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-UM-1998
FRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 172118/1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 7. Application US/08776971B
: Fatent No. 6228984
; GENERAL INFORMATION:
US-39-105-678A-33; Sequence 33, Application US/39105678, Parent No. 6103882. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 46466
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 33:
SEQUIENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fukusumi, Shoji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hinuma. Shuji
Habata, Yugo
                                                                                                                                                                                                                                                                                           130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Conlin, David G. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                 Boston
                                                                                                                                                                                                                                                                                                                                                                                      02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-105-678A-33
                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-776-971-7
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FILING DATE: 28-DEC-1996
APPLICATION NUMBER: UP 7/341371
APPLICATION NUMBER: UP 7/341371
FILING DATE: 18-DEC-1996
APPLICATION NUMBER: UP 8/5919
FILING DATE: 12-AuG-1996
APPLICATION NUMBER: UP 8/21805
FILING DATE: 12-AuG-1996
FILING DATE: 13-SEP-1996
      APPLICATION NUMBER: US/09/421, 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 1, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Habata, Yugo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-421-208-33
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Sequence 33, Application US/09421208
Patent No. 6258561
GENERAL INFORMATION:
APPLICANT: Succaga, Masato
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nichimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guery Match 100.0%; Score 172; DB 3; Length 33; Best Local Similarity 100.0%; Pred. No. 1.4e-19; Matches 31; Conservative 0; Mismatches 0; Indels
CUUNIKI: UGA
ZIE: Q109
COMPUTER RAADABLE FORM:
KEDIUM TYPE: Diskette
COMPUTER: INV compatible
SOFTWARE: FACESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,9718
FILING DATE: 06-Feb.1997
APPLICATION NUMBER: UP 8/59419
FILING DATE: 18-DEC-1996
APPLICATION NUMBER: UP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: UP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: UP 8/246573
APPLICATION NUMBER: UP 8/246573
APPLICATION NUMBE
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #i.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

COLECUE TYPE: protein

FRAGMENT TYPE: incernal

SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-776-971-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 33 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-421-208-33
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Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
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STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Scoke 172; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.4e-19;
Matches 31: Conservative 0; Mismatches 0; Indois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: Ibm compariile
COMPUTER: Ibm compariile
COMPUTER: BastsEQ for Windows Version 2.C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06.Feb-1997
CLASSITICATION: <UNKnown;
PRIOR APPLICATION NUMBER: PCT/JP96/03821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
TILING DATE: 26-UTN-1998
PPLICATION NUMBER: UF 172118/1997
FILING DATE: 27-UTN-1997
ATTORNEY AGENT INPORMATION:
NAME: CONTIN. DAVIG G.
REGISTANTION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION SEC 10 NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
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Gaps

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Ouery Match 100.0%; Scoke 172; DB 3; Length 98; Best Local Similarity 100.0%; Pred. No. 3.1e-19; Matches 31; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                     23 SRAHQHSMEIRTPDINDAWYAGRGIRPVGRF 53
                                                                                                                                              MOLECULE TYPE: procein FRAMENT TYPE: procein SEQUENCE DESCRIPTION: SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: November 12, 2003, 1|:10:39 Job time : 22 secs
    TELEPHONE: 617-523-3400
                     TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
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Kitada, Chieko
TITLE OF INVENTION POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, ELP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                              Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 172; DB 3, Sength 9.
Best Local Similarity 100.0%; Pred. No. 5.1e-19;
Matches 31; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: 18M comparable
COMPUTER: 18M comparable
SOFTWARE: FASTSEO for Wandows Version 2.C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/776.9713
FILING DATE: 66-F65-1997
CLASSIFICATION: <ur
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PRIOR APPLICATION NUMBER: PCT/JP96/03821
FILLING DATE: 28-DEC-1996
APPLICATION NUMBER: UP 7/34331
FILLING DATE: 28-DEC-1995
APPLICATION NUMBER: UP 8/59419
FILLING DATE: 15-MBR: 19 8/59419
FILLING DATE: 15-MBR: UP 8/211805
FILLING DATE: 12-AUG-1996
APPLICATION NUMBER: UP 8/246573
FILLING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 SRAHCHSMEIRTPDINPAWYAGRGIRPVGRF 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
              NAME: CONIE, David G.
REGISTRATION NUMBER: 27,326
REFERENCE/DOCKER NUMBER: 47176
TELECONALNICATION: NIPORKATION:
TELEFAN 617-52:3406
INFCRNATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTR: 98 maino acids
TYPE: maino acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
                                                                                                                                                                                                                                                               TOPOLOGY: Inear
MOLECULE TYPE: protein
FRAGNENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-776-971-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 44, Application US/087769718
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuj:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fuji, Ryo
Fukusumi, Shoji
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MA
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US-08-776-971-44
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AC NO: US-08-776-971
Pat NO: 6228984; Safebook: Assed Potent AA
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ADDRESSEE: DIKE, ERONSTRIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Mater Street
CITY: Boston
                                                                                                                                                                                      COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FactSEQ for Windows Version 2.0
CURSENT APPLICATION DATA:
PILING DATE: 06-Feb-1997
CLASSIFICATION: «Unknow=>
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/JP96/0382:
RILLING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 1/34371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Bingle
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID, NO: 5:
US-08-776-971-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER; 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 617-523-6440 INFORMATION POR SEQ ID NO: 5:
                                                                                                                                                                      MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                 COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-971-97
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                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimmy of Description APPLICANT: Nishimmy of Description APPLICANT: Nishimmy of Description APPLICANT: Nishimmy of Description APPLICANT: Nishimmy of Description Nishimmy Description APPLICANT: ADDRESSEE: DIKE, PRONITEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER EAGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-UN-1998
PRIOR APPLICATION NUMBER: UP 17P118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INPORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27.02
REGISTRATION NUMBER: 27.02
REGISTRATION NUMBER: 27.02
1 SRAHONSMEIRTPDINPAWYAGRGIRPYGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRAHOHSMEIRTPDINPAWYAGRGIRPVERF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 44466-342
TELECOMMUNICATION INFORMATION:
TELEPRONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                      Sequence 31, Application US/09105678A
Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / MOLECULE TYPE: peptide US-09-105-678A-31
                                                                                                                                                                                                                                                                                                                                                               E: DIKE, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino
STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02109
                                                                                                                   US-09-105-678A-31
                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
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Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
NUMBER OK SEQUENCES: 140
CORESPONDENCE ADDRESS:
ADDRESKEB: DIKE, BRONSTEIN, ROBERTS & CUSNMAN, LLP
STREET; 130 Water Stredt
100.0%; Score 172: DB 3; Length 31: 100.0%; Pred. No. 1.3e-19;
                                       Indels
                                                                                                  1 SRAHQNSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                        1 SRAHONSMEIRTPDINPAWYAGRGIRPVGRF 31
                                     Mismatches
                                                                                                                                                                                                        ; Sequence 97, Application US/08776971B; Patent No. 6228984; GENERAL INFORMATION:
                                 0
                                     31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
STATE: MA
COUNTRY: USA
             Best Local Similarity
Matches 31; Conserva
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Fukusumi, Shoji Kitada, Chieko TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE CORRESPONDENCE: 140 CORRESPONDENCE ADDRESS:

Kawamata, Yuji Hosoya, Masaki Fujii, Ryo

Sequence 5, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:

US-08-776-971-5

APPLICANT: Hinuma, Shuji

Habata, Yugo

procein

Run cn:

Sequence:

Searched:

Database

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Bovine G protein-c Bovine pituitary-d

Peptide production Peptide production

Bovine CRH releasi Peptide production Bovine G protein-c Bovine pituitary-d

Bovine oxytodin se

Bovine oxytocin se 1992 ilgand peptid Bovine CRH releasi Peptide production Bovine genome deri Bovine G protein-c

Bovine genome-driv Bovine pituitary-d

Bovine genome-deri

Bovine oxycoin se Bovine oxycoin se Bovine CRH releasi Bovine CRH releasi Projactin releasit briggil peptide, u Rat type ligand po Rat type ligand po Rat 19P2 ligand po Murine pituitary-d Murine pituitary-d Rat oxytodin secre Rat projactin-rele 19P2 ligand poptid Rat oxytodin releasing

Prolactin releasin Rat PrRP-31 peptid Peptide production

Hosoya M:

Result Š

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G prolein-coupled receptor; ligade binding; pharmaceutical;
modulator; pituitary; central nervous system: panereas: prophylactic;
therapeutic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bowine G protein-coupled receptor ligand peptide fragment 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fukusumi S, Habata Y, Hinuma S,
Y, Kitada C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                         AAB73370
AAW31384
AAW97233
AAW87614
AAW95173
                                     AAW95189
AAB10348
AAG62517
ABU60832
                                                                                                                                                                                                                                                                                                                                                                                              AAWS174
AAB10355
AAY87504
AAY49292
AAG62524
AAB90993
AAEZ6400
                                                                                                                                       AAY49297
AAG62518
ABU60833
                                                                                                                                                                                AAW31382
AAW31368
AAW97224
                                                                                                                                                                                                                          AAW97217
AAW95187
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AAG62515
AAG62522
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AAWS
AAB1
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95JP-0343371.
96JP-0059419.
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4449
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28-DEC-1995;
15-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9724436-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawamata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus.
AAW31371:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fujii R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine pituitary-d
Bovine 19P2 ligand
Bovine pituitary-d
Bovine oxycocin se
19P2 ligand peptid
19P2 ligand peptid
Bovine CRH releasi
Bovine PRRP-31 pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovine G protein-c
                                                                                         November 12, 2003. 11:04:47; Search time 41 Seconds (without alignments) 120.013 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                     A Geneseq 19Jun01:*

| SIDSI/geddata/geneseq/genesegp-embl/AA1980 DAT:*
| SIDSI/geddata/geneseq/geneseqp-embl/AA1980 DAT:*
| SIDSI/geddata/geneseq/geneseqp-embl/AA1981 DAT:*
| SIDSI/geddata/geneseqfy-embl/AA1981 DAT:*
| SIDSI/geddata/geneseqfy-embl/AA1981 DAT:*
| SIDSI/geddata/geneseqfy-embl/AA1981 DAT:*
| SIDSI/geddata/geneseqfy-embl/AA1981 DAT:*
| SIDSI/geddata/geneseqfy-embl/AA1980 DAT:*
| SIDSI/geddata/geneseqfy-embl/AA1990 DAT:*
| SIDSI/geddata/geneseqfy-emblembl/AA1990 DAT:*
| SIDSI/geddata/geneseqfy-emblem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                          Compugen Ltd
                                                                                                                                                                                 1 SRAHÇHSMEIRTPDINPAWYAGRGIRPVGRF 31
           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compug
                                                                                                                                                                                                                                                                               Total number of hirs satisfying chosen parameters:
                                                                                                                                                                                                                                                     :107863 segs, 158726573 residues
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                                                                                                                                                                                                                                                                                                                                                   Minimum Match 0%
Maximum Match 190%
Listing first 45 summaries
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AAW95188
AAB10347
AAY49290
AAY49298
AAG62516
                                                                    - protein search, using sw model
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                                                                                                                                                                                                           BLCSUM62
Gapop 10.0 . Gapex= 0.5
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Maximum DB seq length: 200000000
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20
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172
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                                                                                                                                                      Title:
Perfect score:
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Bovine picuitary-derived ligand: modulation; prolactin secretion; de protein-coupled receptor; GPCR; hypowarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid: nypometabolism; lactation; piculiary adenomatosis; brain tumour; emenlopathy; autoimmune disease; prolactinoma; infertility; impotence; amenoribas; gardoromatosis; brain the syndrome; amenoribas; gardorome; corbracally; Chiari-Frommel Syndrome; Argonz-del Castilo syndrome; Porbes-Albrigh; syndrome; lymphoma; Sheehan syndrome; dyscospermia; contraceptive; placential function; choriocarcinoma; hyderid mole; abortion; unthhility fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sovine pituitary-derived ligand polypeptide fragment.
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                                                                     Claim 2; Page 160; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW97218 standard; peptide; 31 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-JPC2765
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                                                                                                                                                                                                                                                                                                                                                                                31, Conservative
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WPI: 1997-363672/33.
                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                 31 AA:
           N-PSDB, AAV02394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUN-1997;
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31 AA;

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prolactions. Infertility, imporence, amenorrhes, galactorrhes. accomegaly, Chiari-Frommel syndrome, Argorated. Castilo syndrome. Stock accomegaly, Chiari-Frommel syndrome, Argorated castilo syndrome. Forbes-Albright syndrome, lymphona, Sheehan syndrome or dystoospermia. The inhibitory agents can also be used as contraceptives. The agents for additating placemental function can be used for treating or preventing choricarcinome, hydatid mole, intuption mole, aboution, unthrifty fetus, abnormal saccharometabolism, abnormal inpidmetabolism or oxylocia.
                                                                                                                                                                                                                                                                                                       The present sequence represents a bovine pirutary-derived ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor IGPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypometabolism, genecyst cacegenesis, menopausa syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing prituitary adenomates; brain tumour, emmeniopathy, altoimmune disease.
                                                                                                 Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, ie.g. for treating menopausal syndrome, tumours, autoimmune didease or abnormal pregnancy
                                                                                                                                                                                                                                           Claim 3; Page 135; 241pp: English
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                                                                                                                                                                                                                                                              This sequence represents a peptide fragment of a novei bovine pituitary derived ligand corresponding to amino acid residues 23 to 53 of the sequence ligand corresponding to amino acid residues 23 to 53 of the sequence in AAW1186 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical Compositions containing this ligand may be used as a pituitary function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for demental, depression, hyperkinetic syndrome, therapeutic agent for demental, depression, hyperkinetic syndrome, charapeutic agent for demental, depression, hyperkinetic syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper-and polyphagia, trauma, syndrome, neurosas, neuerre parcreatitis, renai disease, hyperpolacinaemia, diabetes, cancer. parcreatitis, renai disease, hormone stransiem; syndrome, spinocerebellar degeneration, bone fracture, trauma, atopic dermailis, osteoporosis, asther, epilepsy, inferzility and/or oisgogalactia, assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein.
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                                                                                                        Ligand peptide for 3 protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%: Score 172; DB 18; Length 31; 100.0%; Pred. No. 1.1e-18;
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Gaps
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                           ö
                                                                                                                                                                                                                                  19P2 ligand, G protein coupled raceptor; pituitary; prolactin releasing peptide; catule, dementia; hreast cancer;
Length 31;
                           Inde:s
100.0%; Score 172; DB 20;
100.0%; Pred. No. 1.1e-18:
ive 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Tanaka Y;
                                                  1 SRAHOHSMEIRTPDINPAWYAGRÖIRPVGRF 31
                                                                   1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                  Suenaga M.
                                                                                                                                      AAW87613 standard; Peptide; 31 AA
                                                                                                                                                                                                                                                                                                                                                           98EP-0111725.
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                                                                                                                                                                                      29-MAR-1999 (first entry)
              Best Local Similarity 100.
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  Moriya T, Nishimura O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-047884/05.
                                                                                                                                                                                                              Bovine 19P2 ligand.
                                                                                                                                                                                                                                                                                                                                                                                  27-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                            25-JUN-1998;
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                                                                                                                                                                                                                                                                                     Bos taurus.
                                                                                                                                                              AAWB7613;
 Query Match
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                                                                                                                           AAW87613
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Claim 5; Page 34; 56pp; English.

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Pitultary-derived ligand polypeptide; G-protein coupled orphan receptor; PSPRIG: UPHR-1; modulator; pitultary, central nervous system; pancreas; cissue: screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Muntingion's disease; daug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal; bovine.
             This is the amino acid sequence of the bovine pituitary G protein-coupled receptor ligand 19P2L. A method suitable for commercial high-level production of 19P2L comprises expressing the ligand in host cells as a recombinant fusion protein e.g. with human basic fibroblast growth factor (see AAV81392-93) that has been modified to include an N-terminal cysteine residue. The ligand is released from the fusion by cyanylation followed by amonolysis. 19P2L has prolactin secretion-stimulating and (at migh doses) prolactin secretion-inhibiting properties. It can be used in the treatment and prevention of various diseases including senile dementia. cerebrovascular dementia, and dementia associated with genealogical disorders (e.g. Aizheimer's disease, Parkinson's disease, Pick's disease, Huntington's disease), infectious diseases to creuzfeldt-Jakob's), endocrine or metabolic disease or toxicosis (e.g. hypothyroidism, vitamin Bl2 deficiency, alcoholism, intoxication by drugs, metal and organic compounds), tumourigenic siseases (e.g. chronic cubarachnoidal heamcrinage, and other types of dementia, depression, hyperactive child syndrome (microencephalopathy) and disturbance of consciousess.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               breast cancer, infertility, impotence and autoimmune disease (hypersecretion disorders), and seminal vesicle hypoplasia. Steeporosis, menopausal syndrome and renal failure (hyposecretion disorders.) The 1922 polypetide/amide is also useful as a test reagen: for study of the prolatein secretory function or as a lactogogue in mammalian farm animais.
                                                                                                                                                                                                                                                                                                                                                                                                                                     consciousness. It is also useful for prevention and treatment of diseases associated with prolactin hypo and hypersecretion respectively, including: hyperprolactinaemia, pituitary adenoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 172; DB 20;
100.0%; Pred. No. 1.1e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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les 31; Conservative
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(TAKE) TAKEDA CHEM IND LID.

Pukusumi S, Hinuma S,

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The invertion relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or URF.1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant containing the ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, celral nervous system, pancreas and other cisaues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a collypeptide to the receptor; to quantify the amount of receptor in a collypeptide to the receptor; to quantify the amount of receptor in a collypeptide to the receptor; panched to the receptor; or e.g. to treat senile dementa; Alzheimer's, Parkinson's or Huntington's collabetes; schizophrenia; disorders of growth hormone secretion: cancer; cheumatoid arthritis, epilepsy and many others, also to improve post. Transgenic antuitional status and as vasopressor. Transgenic animals correction of the polypeptide-expressing genes, as models of disease, to disease, to dispeptide bNA is used as a source of cell lines. The ligand collabetes and para source of cell lines. The ligand containsers, in drug development; for gene therapy and to develop transgent animals. The present sequence represents a bovine genome-derived ligand collabetide fragment which is similar to the mirine ingand-polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovine; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure: cow; caesarean section; artificial fertilization; galactostasis: goat; pig; veterinary medicine: milk production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                        for orphan G protein coupled receptors - used of central nervous system, pituitary and
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Pred. No. 1.16-18;
; Mismatches 0:
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                                                                                                                   Example 19; Page 150; 206pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB10347 standard; peptide; 31 AA
                                     New polypeptide ligand for orphar
for treating disorders of central
pancreas, and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matsumoto H, Kitada C, Hinuma
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WPI; 1999-009423/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 AA;
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us-09-446-543a-5.rag

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                                                                                                          This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of druge for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placent, therine recovery failure, casearean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a bovine peptide which acts as an oxytocin secretion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis to to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory
 Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytopin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monoclonal antibody, 1972 ligand: diagnosis, prolactin secretion, pituitary, regulatory mechanism, central nervous system; pancreatic.
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                                                                                                                                                                                                                                                                                                                        100.0%; Score 172; DB 21;
100.0%; Pred. No. 1.1e-18;
1ve 0: Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New monoclonal antibodies, useful in diagnosis, studying diseases related it ligand abnormality
                                                                                                                                                                                                                                                                                                                                                                                                            1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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Physiologically-active polypeptide
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                                                                                 Claim 3: Page 50; 72pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY49290 standard; peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19P2 ligand peptide fragment.
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                                                                                                                                                                                                                                                                                                                                                           31; Conservative
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                                                  medicine
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mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAY49290-102 represent peptide fragments of the 19P2 ligand.
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derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides a monocional antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central mervantse. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative Sequences AAY49290-302 represent peptide fragments of the 19P2 ligand.
                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                             Monoclonal antibody; 19P2 ligand; diagnosis: prolactin secretion;
pituitary; regulatory mechanism; central nervous system: pancreatio.
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                                                                                  Length 31,
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                                                     100.0%; Score 172; DB 21;
Pred. No. 1.1e-18;
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ilarity 100.0%; Préd. No. 1.1e-18;
Conservative 0; Wismatches C.
                                                                                                                                      1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGRF 31
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                                                                                                                                                   1 SRAEQHSMEIRTPDINDAWYAGRGIRPVGRF
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                                                                                    100.0%; FEY
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                                                                                                                                                                                                                                   AAY49298 standard, peptide, 31
                                                                                                                                                                                                                                                                                                                   19P2 ligand peptide fragment.
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                                                                                                           31; Conservative
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                                                                                               Local Similarity
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Matches 31; Conserv
                                                       31 AA;
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                                                                               Query Match
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28-APR-2000; 2000US-0560915.
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Best Local Similarity 100.
Matches 31; Conservative
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                                                                                                                                                              CIVELLE O.
LIN S.
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                                         US2002037533-A1.
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                                                                     28-MAR-2002
               Bos taurus.
                                                                                                                                                                                                          Civelli O,
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                                                                                                                                                     Cow; corticotrophin releasing hormone; CRH; G protein receptor ligand; analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; Addison's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wakefulness, sleep disorder, prolactin releasing peptide receptor; PrRP, GPR10, therapy, epilepsy, narcolepsy, sleepiness; sleep apnoea; insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure; anticonvulsant; bovine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of G protein receptor ligand or peptide for controlling corticotropin releasing hormone secretion -
                                                                                                                         Bovine CRH releasing protein related peptide SEQ ID NO. 3.
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100.0%; Pred. No. 1.1e-18;
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                                  AAG6251£ standard; peptide; 31 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ciaim 3; Page £3; 90pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
                                                               AAG62516;
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      RESULT 8
AAG62516
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                                                                                                                                                           The present invention relates to a method of screening for compounds administering a project or sleep in a mammai. The method involves administering a project releasing peptide (PTRP) receptor (GTR10) agonist or antagonist respectively and determining the ability of the compound to promote wakefulness or sleep. The compounds identified associated with absence seizures and n promoting wakefulness and sleep in individuals having sleep disorders such as insomina and marcolepsy in individuals having sleep disorders such as insomina and marcolepsy to sleeptor agonists may be used to treat common disorders which lead and psychogenic hypersomnia marcolepsy idiopathic hypersomnia and psychogenic hypersomnia such as adjustment sleep for promoting sleep and for treating insomina such as adjustment sleep.
Screening for compounds useful for promoting wakefulness or sleep, and for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep apnea, comprises administering a prolactin releasing peptide agonist or
                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorder and psychophysiologic insomnia. The present sequence is bovine
PrRP-31 peptide.
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                                                                                                                      Disclosure; Page 24; 35pp; English
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Length 31;

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This sequence represents a peptide fragment of a novel bovine pituitary derived ligand corresponding to amino acid residues 23 to 54 of the sequence in AAM31368 and is used in a sasay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, chirapeutic agent for dementia, depression, hyperkinetic syndrome, crimical compositions, trauma, growth hormone secretory disease, hyper and polyphagia, trauma, growth hormone secretory disease, hyper and polyphagia, trauma, hyperplolectionemia, diabetes, cancer, pancreatics, renal disease, hyper architects, spinal injury, transient brain ischaemia, amylotrophic lateral sclerosis, acute
  precursor protein. The method is for producing (low-molecular; peptides edg. KiSS-1 peptide and GRRB ligard for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites. With this method, peptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G protein-coupled receptor; ligand binding; pharmaceutical:
modulator; pituitary; central nervous system: pancreas; prophylactic;
therapeutic agent.
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', Kitada C;
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                                                                                                                                                                                        31 AB;
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12-AUG-1996;
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                                                                                                                                                                                                                                                                                        The invention describes a method of producing a peptide comprising the excision of the N and C-terminals of a target peptide with enzymes or chemically through the artached cleavage sites repeated by ligation in a precursor protein. The method is for producing (low-molecular) peptides e.g. KiSS-1 peptide and GPRB ligand for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with Specific Cleavage sites. With this method, peptide production can be carried out easily to provide iarge quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention.
                                                                                                                                                              and for
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                                                                                                                                                       Process for producing peptides e.g. KiSS-1 peptide and GPRB ligand subsequent applications by gene recombination technique through tan repeats to provide precursor protein with specific cleavage sites
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Pred. No. 1.1e-18;
0; Mismatches 0;
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                                                                                                                                                                                                                                                  Disciosure; Page 58: 87pp: Japanese.
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l Similarity 156.0%;
31; Conservative 5;
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                                                                   Suenaga M,
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                                                                                                           WPI; 2003-129302/12
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ABU60831;

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The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled crphan receptor designated GPR30 (human) or UHR1 (raz). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant the ligand polypeptide, and its fragments. modulate Europhyseptide of Ligand polypeptide, and its fragments. modulate to the pituitary, central nervous system. parcreas and other ciseues and can be used to screen for agents that modulate binding of the polypeptide to the receptor: to quantify the amount of receptor in a compart of and to raise antibodies. They may also be used therapeutically, e.g. to treat senile dementia, Alzheimer's, parkinson's or Huntingion's diseases, Creuzfeld-Jakob disease; poisoning by heavy metals or drugs; contents of arthitis, epilepsy and many others, also to improve post. Theumatoid arthritis, epilepsy and many others, also to improve post. Coperative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPRIO: URR-1; modulator; pituitary; central nervous system; pancreas; tissue; soreen: therapeutlo; binding; senile dementia; ligand; murine: Alzheimer's disease; Parkinson disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer: rheumatoid arthritis; epilepsy; vasopressor;
                     trauma, atopic dermatitis, ostecporosis, asthma, epilepsy, infertility and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein.
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myocardial infarction, spinocerebellar degeneration, bone fracture.
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                                                                                                                                                                       Length 32;
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                                                                                                                                                                     Score 172; DB 18;
Pred. No. 1.2e-18;
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disease, for drug screening and as source of call lines. The ligand polypeptide DNA is used as a source of probes and primers; to identify related sequences; in receptor-binding assays: for production of Ab and antisera; in drug development; for gene therapy and to develop transgenic animals. The present sequence represents a bovine genome-derived ligand polypeptide fragment which is similar to the murine ligand-polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovine, oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure: cow; caesarean section; artificial fertilization; galactostasis: goat; pig:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in vectorinary medicine for promoting milk production in cow, goat and pig. This sequence represents a bovine peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin. as drugs for diseases relating to oxytocin secretion and in veterinary
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100.0%; Pred. No. 1.2e-18;
live 0; Mismatches 0:
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Mismatches
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100.0%; Pred. No. 1.
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The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypodaremocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adread gland hypofunction and obsestry. The
                                                                                                                                                                                                                                                       Cow; corticotrophin releasing hormone, CRH; G protein receptor ligand; analgesic; hyperaldosteronism: hypercortisolaemia; hypoadrenocorticism; Addison's disease; adrena; gland hyperfunction; obesity.
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                                                                                                                                                                                                                     Bovine CRH releasing protein related peptide SEQ ID NO: 4.
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SRAHCHSMEIRTPDINPAWYAGRGIRPVGRF 31
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                                                                                                                    AAG62517 Standard; peptide; 32 AA
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26-SEP-2000; 2000JP-0297073.
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GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
APPLICANT: Lin. Seven
ITILE OF INVENTION: Screening and Therapeutic Methods For TILE OF INVENTION: Promoting Wakefulness and Sleep
FILE REFERENCE: P-UC 4679
CURRENT APPLICATION NUMBER: PCT/USO2/24248
CURRENT FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: US 09/560,915
PRIOR FILING DATE: 2000-64-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4:5
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US-09-1105-678-7
US-09-1205-678-7
US-09-403-6395-39
US-09-403-6395-39
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US-09-403-6395-39
US-09-576-290-97
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PCT-US02-24248-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 13
LENGTH: 31
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 Sequence 13, Appl
                                                                                                                                                   {withous alignments}
163.997 Million cell updates/sec
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                                                                                                                             November 12, 2003, 31:08:23 ; Search time 172 Seconds
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(GDTZ_6/ptodata/1/paa/PCTUS_COMB.pep:*
2: / CGDTZ_6/ptodata/1/paa/US06_COMB.pep:*
4: / CGDTZ_6/ptodata/1/paa/US08_COMB.pep:*
5: / CGDZ_6/ptodata/1/paa/US08_COMB.pep:*
6: / CGDZ_6/ptodata/1/paa/US08_COMB.pep:*
7: / CGDZ_6/ptodata/1/paa/US09_COMB.pep:*
7: / 
                 GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                         172
1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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Total number of bits satisfying chosen parameters:

seq length: 0 seq length: 200000000

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Post-processing: Minimum Match O% Maximum Match 100% Listing first 45 summaries

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5728757 segs, 909918778 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

US-09-446-543A-5

Title: Perfect score:

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SUMMARIES

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US-09-40-4394-39
Sequence 39, Application US/09403639A
Sequence 39, Application US/09403639A
Sequence 39, Application US/09403639A
Sequence 39, Application US/09403639A
SPELICANT: Hinuma, Shuji
TITLE OF INVENTION: Polypeptides, their Production and Use FILE REFERENCE: 2463USOP
CURRENT APPLICATION NUMBER: US/09/403.639A
CURRENT FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: PCT/JP96/61923
PRIOR APPLICATION NUMBER: UP 9-10974
PRIOR PILING DATE: 1997-04-28
NUMBER OF SEQ 1D NOS: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 31:
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                                                               COMPUTER: Eloppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
SOFTWARE: Patentin Release #1.[0, Version #1.30
SOFTWARE: Patentin Release #1.[0, Version #1.30
SOFTWARE: Patentin Release #1.[0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/105,678
FILING APPLICATION NUMBER: US 172118/1997
FILING DATE: 25-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REFERENCE/DOCKET NUMBER: 48466-342
FELEPHONE: 617-523-440
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TTEMPOTH: 31 amino acids
TTEMPOTH: 31 amino acids
TTEMPOTH: 31 amino acids
TTEMPOTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Scdre 172; DB 15:
100.0%; Pred. No. 9.1e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 3:, Conservative
                         ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLSCULS TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS
       COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-403-639A-39
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US-09-403-639B-39
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SEQ ID NO 39
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APPLICANT: Moriya, Takeo
APPLICANT: Mostiva, Takeo
APPLICANT: Tanaka, Yeko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: JIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Stenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Mishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA

ZIP: 02109
COMPUTER 102109
COMPUTER TABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0. Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/39/105,678
FILING DATE: 26-UUN-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JS-JUN-1999
PILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match: 100.0%; Score 172; DB 15: Best Local Similarity 100.0%; Pred. No. 8.1e-17: Matches 31; Conservative 0; Mismatches 0;
1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                             I SRAHOHSMEIRTPDINPARYAGRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: COLLIN. David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION:
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31, Application US/09105678 GENERAL INFORMATION:
                                                                                                                                                                     Sequence 7, Application US/09105678 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 617-523-340
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-105-679-7
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                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 130 W
CITY: Boston
STATE: MA
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US-09-105-678-31
                                                                                                                  RESULT 2
US-09-105-678-7
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Length 31;
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APPLICANT: Kawamata, Yuji
APPLICANT: Kawamata, Yuji
APPLICANT: Hosya, Masaki
APPLICANT: Fuji, Ryo
APPLICANT: Fukusumi, Shoji
APPLICANT: Fukusumi, Shoji
APPLICANT: Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                             Query Match 100.0%; Scoke 172; DB 18:
Bes: Local Similarity 100.0%; Pred. No. 8.1e-17;
Matches 31; Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPERATING SYSTEM: DOS
SOFTWARE: FastSBO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/576,290
                                                                                                                                                                                                                                                                                                                                                                       1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                  1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                           JOTHER INFORMATION: DOVING fragment (23-53) US-09-446-543A-5
       JP 9-165437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
PRICK APPLICATION DATA:
PRICK APPLICATION NUMBER: DP 7/343372
FILING DATE: 28-DEC-1995
RICK APPLICATION NUMBER: UP 8/59419
FILING DATE: 15-MAR.1996
FILING DATE: 15-MAR.1996
FILING DATE: 12-MC-1996
FILING DATE: 12-MC-1996
FILING DATE: 12-MC-1996
FILING DATE: 13-MC-1996
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INPERMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: JP 9-
PRIOR FILING DATE: 1997-06-23
NUMBER DF SEQ ID NOS: 99
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 5
LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM compatible CPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Conlin, David G. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDICH TYPE: Disket
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                                                                                                                                         TYPE: PRI
ORGANISM: artificial
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US-09-403-639C-39
Sequence 39, Application US/08403639C
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/403,639C
CURRENT APPLICATION NUMBER: US/09/403,639C
CURRENT APPLICATION NUMBER: US/09/403,639C
CURRENT APPLICATION NUMBER: US/09/403,639C
SURRENT APPLICATION NUMBER: US/09/403,639C
STOR FILING DATE: 1999-10-25
PRIOR FILING DATE: 1999-10-428
NUMBER OF SEC ID NOS: 96
SOFTWARE:
SOFTWARE:
SEC ID NO 39
LENGTH: 31
TYPE: PRT
CORGANISM: Bovine
                APPLICANT: Hinuma, Shuji,
APPLICANT: Fikusumi, Shuji,
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463180P
CURRENT APPLICATION NUMBER: US/09/403,639B
CURRENT APPLICATION NUMBER: DS/09/403,639B
CURRENT APPLICATION NUMBER: PCT/JP98/61923
PRIOR PILING DATE: 1998-04-27
PRIOR PILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NOS: 96
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 172; DB 18; Length 31; Best Local Similarity 100.0%; Pred. No. 8.1e-17; Matches 31; Conservative 0; Mismatches 0; Indels
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APPLICANT: KAMAMATA, Yuji
APPLICANT: KAMAMATA, Yuji
APPLICANT: FUJI, RW.
TITLE OF INVENTION: Prolactin Secretion Modulator
FILE REPERENCE: 2472350P
CURRENT APPLICATION NUMBER: US/09/446,543A
CURRENT FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 100.0%; Score 172; DB 18;
1 Similarity 100.0%; Pred. No. 8.1e-17;
31; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : SRAHOHSMEIRTPDINPAWYAGRGIRPVGRF 31
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PRIOR FILING DATE: 1998-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09446543A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Bovine
US-09-403-639B-39
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US-09-446-543A-5
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Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION PCLYPRCTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                        Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, 1238
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Diskette
COMPUTER: IBM compatible
OPREATING SYSTEM: DOS
OPFWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/716,147
FILING DATE: 17-Nov-2000
CLASSIFICATION: OBJANDAMI>
PRIOR APPLICATION DATA:
                                                                                                      100.0%; Score 172; DB 19;
100.0%; Pred. No. 8.1e-17;
Live 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/d8/776,971B
FILING DATE: 06-Feb-1997
APPLICATION NUMBER: ECT/J996/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/34371
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 12-MG1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 12-805-1996
APPLICATION NUMBER: JP 8/21605
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                         | SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                       1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGRF 31
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NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID :NO: 5:
                                                                                                                                                                                                                                                                                                                                  RESUL: 1.
US-19-716-147-5
; Sequence 5, Application US/09716147
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Habata, Yugo
; Kawamata, Yugi
; Hosoya, Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                       Conservative
  ; STRANDEDNESS: single
; TOPCLOGY: linear
US-09-576-290-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                      Query Match
Best Local Similarity
Matches 31; Conserva
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APPLICANT: Kawamata, Yuji
APPLICANT: Hosoya, Masaki
APPLICANT: Pujii, Rv.
APPLICANT: Pujii, Rv.
APPLICANT: Tatada, Chieko
TITLE OF INVENTION: PCLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, DLP
STREET: 130 Water Street
                                                                                                                                                                                                                              tength 31;
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                         Cuery Match 100.0%; Score 172; DB 19:
Best Local Similarity 100.0%; Pred. Mo. 8.1e-17;
Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                               SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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APPLICATION NUMBER: UP 7/343371
FILING DATE: 28-20C-1995
FILING DATE: 28-20C-1995
FILING DATE: 18-30E-1995
FILING DATE: 15-30E-1996
FILING DATE: 15-30E-1996
FILING DATE: 15-30E-1996
FILING DATE: 12-30E-1996
APPLICATION NUMBER: UP 8/21805
FILING DATE: 12-30E-1996
APPLICATION NUMBER: UP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONILIA, DAVIG G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/576,290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 97, Application US/09576290 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/776.971
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INFORMATION FOR SEQ ID NO: 97:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
                    LENGTE: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOFOLOGY: Ilnear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hinuma, Shuji
APPLICANT: Habata, Yugo
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
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Length 31;
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APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shoji
TILE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR PILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: PCT/JP98/01923
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GENERAL INFORMATION:
APPLICANT: CIVILIA . Olivier
APPLICANT: Lin, Steven
TITLE OF INVENTION: Screening and Therapeutic Methods For
TITLE OF INVENTION: Promoting Wakefulness and Sleep
FILE REFERENCE: P-UC 4679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 172; DB 23;
100.0%; Pred. No. 8.1e-17;
ive 0; Mismatches 0;
                                                                                                                       Sequence 3, Application US/0986885B
GENERAL INFORMATION:
TILE OF INVENTION: Use of Peptide
FILE REFERENCE: 2584W00P
CURREY FILING DATE: 2002-04-17
PRIOR FILING DATE: 1998-12-25
NUMBER OF SEQ ID NOS: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRAHQHSMEIRTPOINPAWYAGRGIRPVGRF 3.
  SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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Larity IOO.0%; Pred. No. 8.1
Conservative O; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/932.161
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 09/560,915
PRIOR FILING DATE: 2000-04-29
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FactSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 39, Application US/10044592 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity 100.0%; P
31; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Bos taurus
US-09-932-161-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 31: Conserv
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Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-10-044-592-39
                                                                               RESULT 12
US-09-868-885B-3
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                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 3
LENGTH: 31
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LENGTH: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 31;
     Length 31,
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                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WEDLUM TYPE: Diskette
COMPUTER: IBX Compatible
FILING DATE: I7-NOV-2000
CLASSIFICATION TANGER: US/09/716,147
FILING DATE: I7-NOV-2000
CLASSIFICATION TANGEMEN
PRIOR APPLICATION TANGEMEN
ch 105.0%; Score 172; DB 21; Similarity 103.0%; Pred. No. 8.1e-17; 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 172; DB 21; Best Local Similarity 100.0%; Pred. No. 8.1e-17; Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATECN DATA:

APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-76b-1597
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: OF 7/343371
FILING DATE: 15-MRA-1996
APPLICATION NUMBER: JP 8/2118C5
FILING DATE: 15-MRA-1996
APPLICATION NUMBER: JP 8/2118C5
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 9/246573
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 9/246573
FILING DATE: JP 3/24/06-1996
APPLICATION NUMBER: JP 9/24/07-1996
                                                                                                      1 SRAHQHSMEIRTPDINDAWYAGRGIRPVGRF 31
                                                                                                                               1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                         Sequence 97, Application US/09716147 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 617-523-6440
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Fukusumi, Shoji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                       APPLICANT: Himuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NC: 97
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                         Best Local Similarity
Matches 31, Conserv
                                                                                                                                                                                                                           RESULT 11
US-09-716-147-97
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  Query Match
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GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
APPLICANT: Civelli, Olivier
TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (FTRP)
FILE REPERENCE: P-UC 3534
GURRENT FILING DATE: 20C2-03-12
FRIOR RAPLICATION NUMBER: US/10/96,777
GURRENT FILING DATE: 20C2-03-12
FRIOR RAPLICATION NUMBER: US/09/560,915
FRIOR RAPLICATION NUMBER: US/09/560,915
FRIOR RAPLICATION NUMBER: US/09/560,915
FRIOR RAPLICATION NUMBER: US/09/560,915
FRIOR FILING DATE: 2000-04-28
SOTTWARE OF SEQ ID NOS: 24
SOTTWARE OF SEQ ID NOS: 24
SEQ ID NO 13
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                                                                                                                                                                                                                                                   Cuery Match 100.0%; Score 172; DB 26; Best Local Similarity 100.0%; Pred. No. 8.1e-17; Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                    1 SRAHQHSMEIRTPDINPAWYAGRSIRPVGRF 31
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PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: JP 9.109974
PRIOR FILING DATE: 1997-04-28
PUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NO 39
LENGTH: 31
TYPE: PRT
ORGANISM: Bovine
US-10-044-592-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
: ORGANISM: Bos taurus
US-10-096-777-13
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US-10-096-777-13
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Search completed: November 12, 2003, 11:13:44 Job time : 173 secs

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Title: Perfect score:

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sequence 15. Appl Sequence 27. Appl Sequence 27. Appl Sequence 16. Appl Sequence 42. Appl Sequence 41. Appl Sequence 17. Appl Sequence 18. Appl Sequence 27. Appl Sequence 27. Appl Sequence 27. Appl Sequence 28. Appl Sequence 29. Appl Sequence 29. Appl Sequence 29. Appl Sequence 29. Appl

Sequence 30, Appl Sequence 4642, Ap Sequence 4, Appli Sequence 4, Appli

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Sequence 13. Application US/C9932161
Patent No. US20020037533A1
GENERAL INCEMATION:
APPLICANT: CIV-011. Olivier
APPLICANT: Lin. Steven
TITLE OF INVENTION: Screening and Therapeutic Methods For TITLE OF INVENTION: Promoting Wakefulness and Sleep.
FILE REFERENCE: PUC 4679
CURRENT FILING DATE: 2001.08-17
PRIOR APPLICATION NUMBER: US 09/560.915
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
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14 US-10-044-592-90
14 US-10-044-592-90
14 US-10-044-592-96
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16 US-10-044-592-86
17 US-10-044-592-86
18 US-10-044-592-86
19 US-10-096-7-115
19 US-10-096-7-116
19 US-10-096-7-116
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18 US-10-096-7-117
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100.0%; Pred. No. 8e-18;
tive 0; Mismatches 0
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US-10-096-777-13
Sequence 13, Application US/10096777
Publication No. US20030171270A1
GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
APPLICANT: Lin, Steven
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Matches 31: Conservative
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ORGANISM: Bos taurus
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US-09-932-161-13
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                                                                                                                                     November 12, 2003. 11:09:38 ; Search time 28 Seconds (without alignments) 190.151 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGRF 31
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US-10-044-592-40
US-10-044-592-41
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US-10-044-592-86
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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PRIOR APPLICATION NUMBER: UF 9-109974
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
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Matches 31; Conservative
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Matches 31; Conserv
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US-10-044-592-41
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                                                                     SOFTWARE:
SEQ ID NO 40
LENGTH: 32
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TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PERP)
FILE REFERENCE: P-UC 3534
CURRENT APPLICATION NUMBER: US/10/396,777
CURRENT FILING TATE: 2002-03-12
PRIOR APPLICATION NUMBER: US/03/560,915
PRIOR FILING DATE: 2000-04-29
NUMBER OF EQ. ID NOS: 24
SOFTWARE: Fast SEQ for Windows Version 4.0
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APPLICANT: Hunma, Shuji,
APPLICANT: Fukusumi, Shuji,
TITLE OF INVENTION: Polypeptides. Their Production and Use
FILE REFERENCE: 245379
CURRENT APPLICATION NUMBER: US/1C/044.592
CURRENT APPLICATION NUMBER: US/05-61-6
FRIOR APPLICATION NUMBER: US/05-61-6
FRIOR APPLICATION NUMBER: DCT/JD98/01923
FRIOR APPLICATION NUMBER: PCT/JD98/01923
FRIOR FILING DATE: 1999-04-27
FRIOR FILING DATE: 1999-04-28
NUMBER OF SEO ID NOS: 96
SOFTHARE:
SEQ ID NO 39
LENGTH: 31
LENGTH: 31
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APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR PILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-04-27
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Best Local Similarity 100.0%; Pred. No. 8e
Matches 31; Conservative 0; Mismatches
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Publication No. US20020143152A1
GENERAL INFORMATION:
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Publication No. US20020143152A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                     7 TYPE: PRT
CORGANISM: Bos taurus
US-10-096-777-13
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Matches 31: Conserv
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US-10-044-592-39
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US-10-044-592-28
Sequence 28, Application US/10044592
Publication No. US20220143152A1
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Fukusumi, Shoji
ITILE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 246302P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT PILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-40-27
PRIOR FILING DATE: 1997-04-28
SOFTWARE:
SEQ ID NOS: 96
                                                                                                                                                                                                                                                                             Sequence 41, Appl.cation US/:0044593
: Dublication No. US2020143152A1
: GENERAL INFORMATION:
: GENERAL INFORMATION:
: APPLICANT: Hinuma, Shuji
: APPLICANT: Hinuma, Shuji
: TITLE OF INVENTION: Polypeptides. dietr Production and Use
: TITLE OF INVENTION: Polypeptides. dietr Production and Use
: TITLE OF INVENTION: Polypeptides. dietr Production and Use
: TITLE OF INVENTION: Polypeptides. dietr Production and Use
: TITLE OF INVENTION: 1999ptides. dietr Production and Use
: TITLE OF INVENTION: 1999-15.10
: PRIOR FILING DATE: 1999-15.10
: PRIOR FILING DATE: 1999-04-27
: PRIOR APPLICATION NUMBER: DF: 17/JP98/(1923)
: PRIOR APPLICATION NUMBER: JP 9-109974
: PRIOR FILING DATE: 1997-04-28
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        Length 32:
                                                       Indels
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     , DB 14:
8.2e-18:
100.0%: Score 172, Di
100.0%; Pred. No. 8.2
Live 0: Wismatches
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                     Length 98;
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APPLICANT: Fukusumi, Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REPERENCE: 2463U62P
CURRENT APPLICATION NUMBER: US/10/04,592
CURRENT FILING DATE: 2002-01.10
PRIOR PILING DATE: 1999-25-10
PRIOR PLING DATE: 1999-25-10
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1997-04-28
NUMBER: OF SEQ ID NOS: 96
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APPLICANT: Hindma, Shuji
TITLE OF INVENTION: Polypeptides. their Production and Use
FILE REPERENCE: 2464US2P
CURRENT APPLICATION NUMBER: US/10/644.592
CURRENT FILING DATE: 2002-01.10
FRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1997-04-28
PRIOR FILING DATE: 1997-04-28
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         Query Match
100.0%; Score 172; DB 14;
Best Local Similarity 100.0%; Pred. No. 2.7e-17;
Matches 31; Conservative 0; Mismatches 5;
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100.0%, Score 172, DB 14,
Best Local Similarity 100.0%, Pred. No. 2.7e-17,
Matches 31, Conservative 0, Nismatches 0;
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                                                                                                         1 SRAHQHSMEIRTFDINPAWYAGRĢIRPVGRF 31
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                                                                                                                                           23 SRAHQHSMEIRTPJINPAWYAGRGIRPV3RF
                                                                                                                                                                                                                                                                     : Sequence 84. Application US/10044592
: Publication No. US20020143152A1
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        > Sequence 86, Application US/10044592
> Publication No. US20020143152A1
; GENERAL INFORMATION:
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US-10-044-592-84
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US-10-044-592-86
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LENGTH: 98
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Sequence 82. Application US/10344592
Publication 0. US20020143152A1
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuj;
APPLICANT: Hinuma, Shuj;
TITLE OF INVENTION: Polypeptides, their Production and Use CURRENT APPLICATION NUMBER: US/1C/044,592
CURRENT FILING DATE: 2022-01-12
PRIOR APPLICATION NUMBER: US/9/403639
PRIOR PILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                             US-10-044-592-38
Sequence 38 Application US/10044592
Publication No. US20020143152A1
GENERAL INFORMATION:
APPLICANT: Hinuma. Studi
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT APPLICANT: APPLICATION UNMER: US/10/044,592
CURRENT FILING DATE: 2032-01-10
                                                                                                                Query Match.
Best Local Similarity 100.0%; Pred. No. 2.7e-17:
Matches 31; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred, No. 2.7e-17;
Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                           1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                               23 SRAHOHSMEIRTPDINPAWYAGRGIRPVGRF 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2022-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1939-25-10
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR FILING DATE: 1938-04-27
PRIOR APPLICATION NUMBER: UP 9-109374
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
                     TYPE: PRT
CACANISM: Murine
US-10-044-592-28
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ORGANISM: Bovine
US-10-044-592-38
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SEQ ID NO 38
LENGTH: 98
LENGTH: 98
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LENGTH: 98
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1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

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Query Match
Best Local Similarity
Matches 29, Conserv
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Best Local Similarity
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        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Rattus
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APPLICANT: Fukusum. Shuji
APPLICANT: Fukusum. Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2454322P
CURRENT APPLICATION NUMBER: US/10/044.592
CURRENT FILING DATE: 1099-25-10
PRIOR FILING DATE: 1099-25-10
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 98:
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Satent No. US20020037533A1
GENERAL INFORMATION:
TITLE OF INVENTION. Steven:
TITLE OF INVENTION: Promoting Wakefulness and Sleep:
FILE REFERENCE: Promoting Wakefulness and Sleep:
FILE REFERENCE: Puc 4679
CURRENT APPLICATION NUMBER: US/09/932,161
CURRENT FILING DATE: 2001-04.78
PRIOR APPLICATION NUMBER: US 29/560,915
PRIOR FILING DATE: 2005-04-28
NUMBER OF SEQ ID MOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 94.8%; Score 163; DB 9; Length 31; Best Local Similarity 93.5%; Pred, No. 1.6e-16; Matches 29; Conservative 0; Mismatches 2, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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100.0%; Pred. No. 2.7e-17;
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23 SRAHOHSMEIRTPDINPAWYAGRGIRPVGRF 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                    Sequence 88, Application US/10044592
Publication No. US20020143152A1
GENERAL INFORMATION:
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Matches 31, Conserv
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TYPE: PRT
ORGANISM: Rattus
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                                                                                   RESULT 11
US-10-044-592-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-096-777-14
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TYPE: PRT
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SEQ ID NO 88
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APPLICANT: Civelli, Olivier
APPLICANT: Lin. Steven
TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Relating To Prolactin Releasing Peptide :PRRP)
FILE REFERENCE: P-JC 3534
CURRENT APPLICATION NUMBER: US/10/096,777
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: US/09/560,915
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTRARE: FastSEQ for Windows Version 4.0
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APPLICANT: FUKUSUMI, Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/1C/644,592
CURRENT FILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-25-10
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1999-04-28
PRIOR FILING DATE: 1997-04-28
SOFTWARE:
SEQ ID NO 4
LENGTHARE:
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ilarity 93.5%; Pred. No. 1.6e-16;
Conservative 0; Mismatches 2; Indels
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Publication No. US202014315241
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: Hinuma. Shuji
TITLE OF INVENTION: Polypeptides, their Production and Use;
FILE REPERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US/403639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 1.5e-16;
0; Mismatches 2:
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/ Publication No. US20020143152Al
/ GENERAL INFORMATION:
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ilarity 93.5%;
Conservative
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PRIOR FILING DATE: 1999-25-10

PRIOR FILING CATE: 1999-25-10

PRIOR FILING CATE: 1996-61-27

PRIOR FILING CATE: 1996-62-27

PRIOR FILING CATE: 1996-62-27

PRIOR FILING CATE: 1996-64-27

PRIOR FILING CATE: 1999-64-28

NUMBER OF SEQ ID NOS: 96

SEQ ID NO 5

LENGTH: 31

TYPE: PRT

NAME/REY: PEPTIDE

LOCATION: (1) . (31)

OTHER INFORMATION: antigen

US-10-044-992-5

Query Match

East Local Similarity 93.5%; Pred. No. 1.6e-16;

Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps

OV I SRAHGHSMEIRTPDINFAWYGGIRPVGRF 31

Db : SRAHGHSMEIRTPDINFAWYGGIRPVGRF 31

Search completed: November 12, 2003, 11:14:55

Job time: 28 secs
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us-09-446-543a-5.rapn

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RESULT 1
US-60-478-196-3124
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Sequence 1500, App
Sequence 1500, App
Sequence 194, App
Sequence 1843, App
Sequence 611, App
Sequence 611, App
Sequence 5285, App
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Sequence 17846, h
Sequence 17224, h
Sequence 51229, h
Sequence 50166, h
Sequence 50166, h
Sequence 50166, h
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10212, A
10845, A
1208, Ap
9397, Ap
12917, A
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68107, A
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                                                                                             (without alignments)
82.426 Million cell updates/sec
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                                                                             November 12, 2003, II:08:48 : Search time 18 Seconds
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(1) / Ggn2 6/ptodata/1/paa/PCT NEW COMB.pep:*

(2) / Ggn2 6/ptodata/1/paa/USO6_NEW COMB.pep:*

(2) / Ggn2 6/ptodata/1/paa/USO8_NEW COMB.pep:*

(3) / Ggn2 6/ptodata/1/paa/USO8_NEW COMB.pep:*
          GenCore version 5.1.6
(c) 1993 - 2003 Compuges Ltd.
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PCT-USC3-3029-394
PCT-USC3-3029-1904
US-10-666-642-1500
US-10-666-642-1500
US-10-679-063-8843
US-10-679-063-5285
US-10-679-063-5285
US-10-679-063-5285
US-10-679-063-10848
US-10-679-063-10848
US-10-425-1144-50129
US-10-425-1144-50139
US-10-425-1144-50166
US-10-425-1144-50166
US-10-425-1144-50166
US-10-425-1144-50166
US-10-425-1143-50168
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US-10-425-114A-68157
US-09-976-858-171
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US-10-679-063-13708
                                                                                                                                                       1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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                                                                                                                                                                                                                  252157 seqs, 47860546 residues
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Maximum Match 100%
Listing first 45 summaries
                                                         protein search, using sw mode.
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                    length: 0
length: 2000000000
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172
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Match Length DB
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Sequence 5703, A
Sequence 5673, A
Sequence 10, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 2, Appl
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Sequence 15278, A
Sequence 461, App
Sequence 463, App
Sequence 6220, App
Sequence 336, App
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Sequence 1908, Ap
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Sequence
Sequence
Sequence
US-10-679-263-21837
US-59-581-286A-432
US-59-581-286A-327
US-10-425-114A-5727
US-10-425-114A-5727
US-10-425-114A-5727
US-10-426-686A-26
US-10-436-686A-26
US-10-478-1563-31
US-10-478-1563-31
US-10-478-1563-31
US-10-478-1563-31
US-10-478-1563-31
US-10-478-1563-31
US-10-478-1563-31
US-10-679-063-13181
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APPLICANT: Jiang, Bo
APPLICANT: Lemieux, Sebastien
APPLICANT: Lemieux, Sebastien
APPLICANT: Moment
APPLICANT: Moment
TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF ASPERGILLUS FUMIGATUS AND
TITLE OF INVENTION: USE
FILE REPRESENCE: 10182-026-888
CURRENT FILLION NUMBER: 2003-06-13
NUMBER OF SEQ ID NOS: 4000
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3124
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US-10-389-647-469
: Sequence 469, Application US/15389647
: Sequence 469, Application US/15389647
: SEQUENCE INFORMATION:
APPLICANT: GENUSTER, Martin
APPLICANT: LOSTROW, CANDER, SENSING
ITLE OF INVENTANCH, CHORGAS
: TITLE OF INVENTANCH, CHORGAS
: TITLE OF INVENTANCH, CHORGAS
: TITLE OF INVENTANCH, CHORGAS
: CURRENT APPLICATION NUMBER: US/10/389,647
: CURRENT FILING DATE: 2003-03-14
: PRIOR FILING DATE: 2000-09-01
: PRIOR FILING DATE: 2000-09-01
: PRIOR FILING DATE: 1999-03
: WUMBER OF SEQ ID NOS: 710
: SSOTWARE: PASESED for Windows Version 4.0
: SSOTWARE: 664
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Pred, No. 9.2.
4: Mismatches 9: Indels
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Sequence 3124, Application US/60478196 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-60-478-196-3124
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Best Local Similarity 43.5%;
Matches 10; Conservative
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PCT-US03-30292-1500
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US-10-666-642-1500
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US-10-666-642-394
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LENGTH: 380
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CURRENT APPLICATION NUMBER: E0/411.837
PRIOR APPLICATION NUMBER: E0/411.837
PRIOR APPLICATION NUMBER: E0/444,166
PRIOR APPLICATION NUMBER: E0/445.809
PRIOR PILING DATE: 2002-12-17
PRIOR PILING DATE: 2003-64-24
NUMBER OF SEQ 1D NOS: 2247
SOFTWARE: PatentIn Version 3.2
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                                                            Query Match 29.9%; Score 51.5; DB 6; Length 664; Best Local Similarity 55.6%; Pred. No. 52; Matches 10; Conservative 2; Mismatches 5; Indels 1
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APPLICANT: SHERMAN, Bradley K
TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 380;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.2%; Score 48.5; DB 1; 35.5%; Pred. No. 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1500, Application PC/TUS0330292
GENERAL INFORMATION:
APPLICANT: Mendel Biotechnology, Inc.
                                                                                                                                                                                                                                                                           Seguence 394, Application PC/TUS0330292 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                               APPLICANT: Mendel Biotechnology, Inc.
                                                                                                                                                                                                                                                                                                                                          JIANG, Car-Zhong
HEARD, Jacqueline E
RATCLIFFE, Oliver
CREELMAN, Robert A
ADAM, Luc Jronne
REUBER, T. Lynne
RIECHMANN, Jose Juis
HAAKE, Volker
: ORGANISM: Pseudomonas aeruginosa
US-10-389-647-469
                                                                                                                                                                           476 VNTPDINP-WELQRSGRP 452
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HEARD, Jacqueline E
RATCLIFFE, Oliver
CREELMAN, Robert A
ADAM, Lus J
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RIECHMANN, Jose Luis
                                                                                                                                           10 IRTPDENPAWYAGRGIRP 27
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PCT-US03-30292-394
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KEDDIE, James S
SHERMAN, Bradley
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Best Local Similarity 35.54
Matches 11: Conservative
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LENGTH: 380
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APPLICANT:
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CURRENT APPLICATION NUMBER: 2003-09-18
PRIOR PRIOR APPLICATION NUMBER: 60/434,166
PRIOR APPLICATION NUMBER: 60/434,166
PRIOR APPLICATION NUMBER: 60/434,166
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Best Local Similarity 35.5%; Pred. No. 60:
Matches 11; Conservative 3; Mismatches
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CURRENT APPLICATION NUMBER: PCT/US(3/30292 CURRENT FILING DATE: 2003-09-22
                                      CURRENT FILING DATE: 2003-09-22
PRIOR APPLICATION NUMBER: 60/411,837
PRIOR PILING DATE: 2002-09-18
PRIOR PRIOR CATION NUMBER: 60/434,166
PRIOR PLING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: 60/465,849
PRIOR PLING DATE: 2003-04-24
NUMBER OF SEQ ID NOS: 2247
SOFTWARE: PatentIn version 3.2
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, GENERAL INFORMATION:
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GENERAL INFORMATION:
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HEARD, Jacqueline E
RATCLIFFE, Oliver
CREELMAN, Robert A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thallana
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Matches 11, Conservative
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; Sequence 62112, Application US/10425114A
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 57.9
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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US-10-679-063-5285
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GENERAL INFORMATION:
1 APPLICANT: Obtain, Yuich:
1 TITLE OF INVENTION: BREAST, GASTRIC, AND PROSTATE CANCER ASSOCIATED ANTIGENS AND
1 TITLE OF INVENTION: USES THEREFOR
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                                         APPLICANT: UJANG, CA1-ZEONG
APPLICANT: HEARD, JCACCELINE
APPLICANT: RATCLIFFE, Oliver
APPLICANT: RATCLIFFE, Oliver
APPLICANT: REUBER, T. Lynne
APPLICANT: REUBER, T. Lynne
APPLICANT: REUBER, T. Lynne
APPLICANT: REUBER, T. Lynne
APPLICANT: RECHE, VANOIG N
APPLICANT: REDBEL, Arnold N
APPLICANT: SHERMAN, Gose Luis
APPLICANT: SHERMAN, Bradley K
ITILE OF INVENTION: POLYMCLeotides and Polypeptides in Plants
FILE REFERENCE: MB1-0054
CURRENT APPLICATION NUMBER: 60/411,837
PRIOR APPLICATION NUMBER: 60/411,837
PRIOR PLILOM DATE: 2002-09-18
PRIOR PLILOM DATE: 2002-09-18
PRIOR PLLING DATE: 2002-09-18
PRIOR PLLING DATE: 2003-09-18
PRIOR PLLING DATE: 2003-04-24
SOFTHARE: PARENTENCE: MUMBER: 60/465,809
LENGTH: 380
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TITLE OF INVESTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 30-15(52054)B
CURRENT APPLICATION NUMBER: US.20/61063
CURRENT PILLING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415.758
PRIOR APPLICATION NUMBER: 60/415.758
NUMBER OF 550 ID NOS: 27373
SEQ ID NO 8843
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US-10-679-063-8843
Sequence 8843, Application US/10679063
GENERAL INFORMATION:
Mendel Biotechnology. Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-666-642-1500
                                 JIANG, Cal-Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Nicotiana alata
US-i0-679-063-8843
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Best Local §
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Solou, Yihua
APPLICANT: Screen, Serven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Color Serven E
APPLICANT: Absolution Worleic Acid Molecules and Other Molecules Associated With IITLE OF INVENTION: Moleic Acid Molecules and Other Molecules Associated With IITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement IITLE OF INVENTION: NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 73128
SEQ ID NO 62112
LENGTH: 234
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TITLE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38 15(52054) B
CURRENT APPLICATION WIMBER: US/10/679,063
CURRENT FILING DATE: 2003-16-02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 5285
LENGTH: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                              27.9%; Score 48; DB 5: Length 117; 57.9%; Pred, No. 39;
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27.9%; Score 48; D8 6;
Best Local Similarity 48.0%; Pred; No. 55:
Matches 12; Conservative 2; Mismatches
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DCATION: (1)..(190)

OTHER INFORMATION: unsure at all Xaa locations

US-10-69-063-5285
CURRENT APPLICATION NUMBER: US/09/999,932A
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/136,526
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: US 60/153,454
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 1332
SOFTWARE: PATENTIN VERSION 3.2
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 611
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27.9%; Score 48; DB 6; 35.0%; Pred. No. 1.2e+02;
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US-10-425-114A-51299
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// GENERAL INFORMATION:
// APPLICANT: Liu, Jingdorg
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US-10-425-114A-50166
Sequence 50166, Application US/10425114A
GENERAL INFORMATION:
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LRTDPVSPTWHSTRGVSEDG 162
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          APPLICANT: Liu, Jingdong
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Best Local Similarity
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays
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TITE OF INVENTION: TRANSCENCE PLANTS WITH IMPROVED PHENOTYPES
FILE REPRENCE: 38-15 ($2054)8
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR PILING DATE: 2003-10-02
PRIOR FILING DATE: 2010-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 10848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1024, Application US/10679063
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSCENIC PLANTS MITH IMPROVED PHENOTYPES
FILE REPERENCE: 38-15(52054)B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 200-10-62
PRIOR PAPLICATION NUMBER: 60/415,758
PRIOR FLING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
LENGTH: 314
                                                                                                                        Score 46; DB 6; Length 234;
Pred. No. 64;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.9%: Score 48; DB 6; Length 314; 32.0%; Pred. No. 80; tive 5; Mismatches 12: Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 27.9%; Score 48; DB 6; Length 293; Best Local Similarity 32.0%; Pred, No. 76; Matches 8; Conservative 5; Mismatches 12; Indels
                                                            : OTHER INSCRMATION: Clone ID: UIB3166-014-B6_FLL:pep
US-10-425-114A-62112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) TYPE: PRT / ORGANISM: Mycobacterium tuberculosis CDC1551 US-10-679-063-10848
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                                                                                                                      Cuery Match
Best Local Similarity 33.3%:
Matches 9: Conservative
TYPE: PRT
CRGANISM: Gossypium hirsutum
FEATURE:
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Best Local Similarity 32.0%
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US-10-679-063-10848
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APPLICANT: Zhou, Yihuaa APPLICANT: Zhou, Yihuaa APPLICANT: Screen, Steven E APPLICANT: Screen, Steven E APPLICANT: Screen, Steven E APPLICANT: Tarbaska, Jack E APPLICANT: Cao, Yongwei TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement File Reference: 38-21(5)313)8 CURRENT APPLICATION NUMBER: US/10/425,114A NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 51299 NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zhou, Yihua APPLICANT: Kovalic, David K. APPLICANT: Kovalic, David K. APPLICANT: Kovalic, David K. APPLICANT: Kovalic, David K. APPLICANT: Screen, Steven E APPLICANT: Tabaska, Jack E APPLICANT: Cac, Yongwei TITE OF INVENITON: Nucleic Acid Molecules and Other Molecules Associated With FILE OF INVENITON: Plants and Uses Thereof for Plant Improvement FILE REPERENCE: 38-21(53313)8
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73:28
SEQ ID NO 60539
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ö
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27.9%, Score 48; DB 6; Length 525
Best Local Similarity 33.3%; Pred. No. 1.2e+C2;
Natches 9; Conservative 5; Mismatches 7; Indels
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US-10-425-114A-60539
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FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US,10/425,114A
CURRENT FILING DATE: 2003-04-25
SEQ ID NO 50166
LENGTH: 541
TYPE: PRT
CORRANTING CORPERENCE: 13128
LENGTH: 541
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Lid.

OM proteir - protein search, using sw model

November 12, 2003. :1:06:47; Search time 2: Seconds [without alignments] 141:963 Million cell updates/sec Run on:

US-09-446-543A-5 172 1 SRAHQHSMEIRIPDINFAWYAGRGIRPVGRF Title: Perfect score: Sequence:

Blosum62 Gapop 12.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 3 Maximum DB seq length: 2200000000

Post-processing: Minimum Match 18 Maximum Match 150% Listing first 45 summaries

PIR_76:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Darabase

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		**			SUMMARIES	
Result No.	Score	Query Match	Lengt	<u>1</u> 38	ID	Description
	. 4	94.8		2	JC7607	prolactin-releasin
2	56.3	12.8	303	7	AH20:6	hypothetical prote
3	55		1236	N	9	Mg protoporphyrin
4	54.5	31.7	503	N	-4	Sun/nucleolar prot
5	ω.	31.1	175	CE	S	hypothetical prote
9	Si B	30.8	376	~	8	aderine deaminase-
7	52		73	~	m	hypotherical proce
∞	52		308	2	8	transcription requ
6	52	30.2	308	~	397672	rok family protein
50	52		419	2	AH3166	hypothetical prote
11	52	30.2	1292	~	T31462	probable madnes:
12	3.13	29.9	664	2	783376	conserved hypothet
13	51	29.7	294	2	T21075	cal prot
14	51	29.7	430	Н	B69009	i hyr
13	51	29.7	796	~	S11210	probable unr prote
16	51	29.7	962	~	H69157	excinuclease ABC c
17	50.≡	29.4	790	7	747959	
8	50		527	N	733175	
19	50	29.1	974	7	AH3361	excinuclease ABC c
20	49.5	28.8	393	~	AB2664	- 5
21	•		401	7	A97446	hypothetical prote
22	49	28.5	128	~	S76955	hypothetical prote
23	49		226	2	A87664	hypothetical prote
24	48.5	28.2	254	~	S76814	
25	48.5		548	~	T47548	hypotherical prote
26		28.2	1882	2	73	
27	4.0		72	2	9100	probable regulator
28	8.4	27.9	220	2	C83292	glut
59	4. 80	27.9	-+	7	7056	hypothetical prote

hypotherical prote	hypothetical prote	acetoacetyl-CoA re	samB protein - Sal	sensory box histid	protoporphyrin IX	excinuc_ease ABC c	ABC excinuclease s	excinuclease ABC c	protoporphyri: IX		protoporphyrin IX	protoporphysic IX	protoporphyrin IX	pretoporphyrin IX	magnesium chelatas
T21648	T39098	JC7675	B38176	D87559	T07958	A71315	AH2762	G97543	AE2351	575000	\$37310	564721	871288	T01789	T07126
N	~	N	~	2	2	~	0	2	N	N	0	N	2	N	2
348	365	197	424	637	772	096	973	982	1328	1331	1379	1380	1381	1382	1383
27.9	27.9	27.9	27.9	27.9	27.9	27.9	27.9	27.9	27.9	۲.		27.9	۲.	27.9	27.9
2	۲.	27.	8 27.	8 27.	27.	8 27.	. 27.	8 27.	27.	27.	27.	27.	27.	B 27.	27.

ALIGNMENTS

projectin-releasing peptide - rat

projectin-releasing peptide - rat

projectin-releasing peptide - rat

projectin-releasing peptide - rat

Cibate: Ratuma norvegicus (Norway rat)

Cibate: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

CiAccession JC7607

R:Yamada, M: Ozawa, A: Eshii, S: Shibusawa, N: Hashida. T: Ishizuka. T: Hosoya.

R:Yamada, M: Ozawa, A: Eshii, S: Shibusawa, N: Hashida. T: Ishizuka. T: Hosoya.

R:Yamada, M: Ozawa, A: Seb.

A; Reference number: JC7607; MUID:21092785; PMID:11178959

A; Residues: Jc7607

A; Molecule type: DNA

A; 0 Gaps ö ch 1 Similarity 93.5%; Pred. No. 6.9e-17; 29; Conservative 0; Mismatches 2: lidels Ouery Match Best Local Similarity Matches 29; Conserv

1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGRF 31 22 SRAHQHSMETRIPDINPAWYTGRGIRPVGRF 52 ठे 쉼

RESULT 2
AH2016
hypothetical protean allie86 [imported] - Nostoc sp. istrain PCC 7:20;
C;Species: Nostoc sp. PCC 7120
C;Sacession: AH2016
E;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu: Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacter:um A;Reference number: AB1807; MUD:21599285: PMID:11759840
A;Status: preliminary
A;References DNA
A;Residues: 1-03 <CMR>
A;Cross-references: GB:BA000019; PIDN:BAB78052.1: PID:g17135506; GSPDB:GNC1179
A;Cross-references: Strain PCC 7120
A;Experimental source: strain PCC 7120

C;Genetics: A;Gene: all1686

Query Match

Length 303; 32.8%; Score 56.5; DB 2; ä

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A;Reference number: $67143
A;Accession: $67150
A;Accession: $67150
A;Accession: $67150
A;Accession: $67150
A;Accession: $67150
A;Cross-references: EMBL:Z75161; NID:q1420572; PID:e252411; PID:g1420573; GSPCB:GN00C
A;Experimental source: strain $288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Molecule type: DNA
A.Residues: 1-376 <WHI>
A.Cross-references: GB:AEC01863; GB:AEC01825: NID:g6450670: PIDN:AF12376.1: PID:g646
A.Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agrist Agristal protein AGR L 109 (imported) - Agrobacterium tumefaciens (strain DS9, Ce C.Species Agrobacterium tumefaciens (of Species Agrobacterium tumefaciens (Species Agrobacterium tumefaciens C.Species Agrobacterium tumefaciens C.Species Agrobacterium tumefaciens C.Species Agristal Agrobacterium Agrefacence Dumber: Agrobacterium Agrobac
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C;Species: Deinococcus radiodurans
R;White, O.; Essen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.
R.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 266, 1571-1577, 1999
A;File: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:2036896; PMID:10567266
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         C;Date: 12-Jul-1996 #sequence_revision i2-Jul-1996 #text_change 19-Apr-2002
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                                                                                                                                                  July 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 30.8%; Score 53; DB 2; Best Local Similarity 40.0%; Pred. No. 6.1; Matches 12; Conservative 6; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 SECHQHNVFVYLPAVDDLTKQWFIAHGFEQVG 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
31.1%; Score 53.5; DB
Best Local Similarity 31.2%; Pred. No. 2.3;
Matches 10; Conservative 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SRAHOHSMEIRTP---DINPAWYAGRGIRPVG
                                                    C.Accession: S67150
P.Jauniaux, C.C.: Poirey, R. submitted to the Protein Sequence Darabase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Genetics:
A.Gene: MIPS.YOR253w
A.Gross-references: SGD:S0005779
A.Map position: 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-73 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CyGenetics:
AyGene: DRA0268
AyMap position:
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C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C.Accession: 482193
R.Heidelberg. C.F.; Elsen, J.A.; Neison, W.C.: Ctayton, R.A.; Gwinn, M.L.; Dodson, R.J.; R.Heidelberg. C.F.; Elsen, J.A.; Nemathevan, J.; Bass, S.; Oin. H.; Dragor, I.; Sellers. F.; R.T.; Mekalanos, J.C.: Verter. J.C.; Fraser, C.M.
Nature 406, 477-493, 2000
Nature 406, 477-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Accession: T50904

**Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K.

**Submitted to the EMBL Data Library, November 1999

**APE ference number: Z25270

**A.Reference  DNA

**A.Reference: DNA

**A.Reference: DNA

**A.Reference: EMBL: ABD34704; PIDN: BAA94057.1

**A.Reference: EMBL: ABD34704; PIDN: BAA94057.1

**A.Reference: EMBL: ABD34704; PIDN: BAA94057.1

**A.Reference: EMBL: ARGalatus magnesium-pro::oporphyzin O-methyitransferase

C.Gene: DchA

**C.Supertamily: Rhodobacter capsulatus magnesium-pro::oporphyzin O-methyitransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mg protoporphyrin methyl transferase [imported] - Rubrivivax gelatinosus
C;Species: Rubrivivax gelatinosus
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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C;Species: Saccharomyces cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 32.0%; Score 55; DB 2:
1 Similarity 34.4%; Pred. No. 11:
11: Conservative 6: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 AHQHSMEIRTPDINPAWYAG-----RGIRPV 28
                                                                                                                                                                                                                              226 HEHSYE-RIRALDGITYLICGAGAGNRPVGR 255
    Pred. No. 1.5;
                                                                                                                                    4 HQHSMEIRTFDINPAWY----AGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 54.5; Di
Pred. No. 5;
6; Mismatches
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                                                    2: Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.7%;
ilarity 36.7%;
Conservative
    51.6%;
Local Similarity 51.63
hes 16. Conservative
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Best Local Similarity
Matches 11, Conserva
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Sest Local Similarity
Matches 11, Conserv
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    Best Loc
Matches
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A; Map position: linear chromosome

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us-09-446-543a-5.rpr

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probable magnesium chelatase (EC 4.99)[1.-] chain H BohH - Heliobacillus mobilis C; Species: Heliobacillus Mulb: 99064957; PMID: 9843979
A; Reference number: 221036; MUID: 99064957; PMID: 9843979
A; Reference number: 221036; MUID: 99064957; PMID: 9843979
A; Residues: Dray A; Residues: Dray A; Residues: L: 222 C; A; Redobacter capsulatus magnesium-protoporphyrin O-methyltransferase C; Reywords: lyase
                                                                                                      CiSpecies: Agrobacterium tumefaciens
CiDate: 11-5an-2002 #sequence_revision 1:-Jan-2002 #text_change 18-Nov-2002
CiAccession: AH3166
R.Yood, D.W.: Setubal. J.C.; Kaul, R.; McDks, D.: Chen, L.: Wcod, G.E.: Chen. Y.; Wco
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.: Levy, R.; Li, M.: McCl
* Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2332, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jing, M.: Krespan, W.; Perry, M.; Gordon-Kam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - Pseudomonas aeruginosa (strain PAC
                                                                             hypothetical protein ugps [imported] - Agrobacterium tumefaciens (strain CS8. Dupont)
                                                                                                                                                                                                                                                                                                                                                                                         sier, E.W.
A.Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CBB.
A.Reference number: AB2577; MUID:21608550: PNID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein PA2151;[imported] - Pseudomonas aeruginosa (straic), Species: Pseudomonas aeruginosa
C.Species: Pseudomonas aeruginosa
C.Date: 15.Sep-2000 #sequence_revision 15.Sep-2000 #text_change 31-Dec-2000
C.Accession: F83376
R.Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.: Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.: Folger, K.R.: Kas, A.: Larbig.: Lory, S.; Oison, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A/Status: preliminary
A/Status: preliminary
A/Molecule type: DDA
A/Molecule type: DDA
A/Residues: 1-419 *KUR>
A/Cross-references: GB:AE008667; PIDN:AAL45750.1; PID:g17743481: GSPDB:GN001g8
A/Experimental source: strain C58 *Cupont)
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Pred. No. 32;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 52: DB;
Pred. Nc. 3.6;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 SPEANATWFAGTGYLPINK 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 TPDINPAWYAGRGIRPVGR 30
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36.8%;
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Best Local Similarity 38.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 36.8'
Matches 7; Conservative
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A;Gene: ugpB
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C(Species: Agrobacterium rumefaciens
C(Species: Agrobacterium rumefaciens
C(Species: Agrobacterium rumefaciens
C(Accession: B972001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C(Accession: B97502 R) (Southing C) (Allinger, M.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Socien, C.; Lappas, C.; Markelz, B.; Science 294, 2324-2338, 2001
A: Rice conce control of the Plant Pathogen and Biotechnology Agent Agrobacterium rumers reference number: A97359; MUID:21608551; PMID:11743194
A: Residues: preliminary
A: Molecule type: DNA
A: Residues: 1-308 KURA
A: Cross-references: GB: AE007869; PIDN: AAK88331.1; PID: gis157809: GSPDB: GN0169
C(Genetics: A) (A128
A: Map position: circular chromosome
C; Superfamily: conserved hypothetical protein H10182: glucose kinase homology
                                                                                                                                                                                                                                                                                                                                                                              transcription regulator, ROX family Atuž609 (imported) - Agrobacterium tumefaciens (stra
C;Species: Agrobacterium tumefaciens
C:Date: il-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C, Accession: A42896
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks. D.; Chen, L.; Wood, G.E.; Chen. Y.; Woo. L
erage, G.; Gliect, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McC.ell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2021
A; Authors: Yoo, B.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Attitle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
Attitle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
Affeterence number: AB2577; MUD:21608550; PMID:11743193
A.Accession: A42836
A.Status: preliminary
A.Molecule type: DNA
A.Residus: 1-308 «KUR»
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C,Superfamily: conserved hypothetical protein H10182; glucose kinase homology
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       Length 73:
                                                                         Indels
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       7
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Best Local Similarity 50.0%; Pred. No. 6.9;
Matches 10; Conservative 2; Mismatches
   Score 52; DB 2
Pred. No. 1.5;
                                                                     3: Mismatches
                                                                                                                                       5 AHQHEMEIRTPDINPAWYAGR 23
                                                                                                                                                                                       23 AHTHRDEVRSACISVRWLAGR 43
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Query Match 30.2%; Best Local Similarity 47.6%; Matches 10, Conservative
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Matches 10; Conserv
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Gaps

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Score 51, DB 1, Length 430, Pred. No. 14: 0; Mismatches 4, Indels

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A:Status: nucleic acid sequence not shown; translation not shown.
A:McJecule type: DNA
A:McSiduses: 1-40 cMTH>
A:McSiduses: 1-40 cMTH>
A:Cross-references: GB:AE000877; GB:AE000666; NID:g2622157; PIDN:AAB85559.1; FID:g262
A:Experimental source: strain Delta H
C:Generias: A:Gene: MTH:070
C:Superfamily: conserved hypothetical ;protein MTH:070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable unr protein - rat
Crispecies: Rattus norvegicus (Norway rat)
Crispecies: Rattus norvegicus (Norway rat)
Crispecies: Rattus norvegicus (Norway rat)
Crispecies: All 1210
R.Jeffers, M.; Paciucci, R.; Pellicer; A.
Nucleic Acids Res. 18, 48919, 1990
A.; Tille: Characterization of unr. a gene closely linked to N-ras.
A.; Reference number: S11210; MUID:90370473; PMID:2204025
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A, Molecule type: mRNA
A, Residues: 1-798 cJEF>
A, Cross-references: EMBL:XS2311; NID:957454; PIDN:CAA36549.1; PID:957455
C, Keywords: DNA binding
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43.5%; Pred. No. 27;
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Best Local Similarity 69.23
Matches 9, Conservative
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Matches 10; Conservative
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                                     ATITIE: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathod A.Reference number: A82956; MJD:20437337; PMID:10984043
A.Accession: F83376
A.Status: preliminary
A.Molecule Type: DNA
A.Residues: L-64 <STO>
A.Cross-references: GB:AE004642; GB:AE004091; NID:g9948163; PIDN:AAG05539.1; GSPDB:GN001
C.Genetics:
A.Gene: PA2:51
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R. Smith, D.R.; Doucette-Stamm, J.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Oliv, D.R.; Doucette-Stamm, J.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Oliv, D. Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S.; Church, G.M.; Daniels, C.J.: Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A.Title: Complete genome Sequence of Methanobacterium thermoautotrophicum Delta H: funct A.Reference number: A69000; MUID:98037514; PMID:9371463
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C:Species: Methanobacterium thermoautotrophicum
C:Date: 29-Jan-1999 #sequence_revision 29-Jan-1899 #text_change 23-Jul-1999
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A:Reference number: Z19378
A:Reference number: Z19378
A:Reference number: Z19378
A:Reference T12124
A:Reference number: Z19378
A:Reference Dray
A:Rolecule type: DNA
A:Reference DNA
A:Reference DNA
A:Reference DNA
A:Reference T1294
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A:Reference number: 219368
A:Reference number: 219368
A:Accession: 121075
A:Accession: 121075
A:Batus: preliminary: translated from GB/EMBL/DD5J
A:Molecule type: DNA
A:Residues: 1.294 <Wll>
A:Residues: 1.294 <Wll>
A:Residues: EMBL: 250875; FIDN:CAA95762.1; GSFDB:GN00228; CESP:F19M6.1
A:Experimental source: Glone F17E5
R:McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2006
C:Accession: T21075, T21124
R:McMurray, A.
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Local Strilarity 44.8%; Pred. No. 9.2;
Los 13; Conservative 2; Mismatches 12; Indels
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Nature 405, 959-964, 2000
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OM protein - protein search, using sw model

November 12, 2003, 11:05:42 ; Search time 11 Seconds (without alignments) 132.520 Million cell updates/sec Run on:

Title: Perfect score: Seguence:

US-09-446-543A-5 172 1 SRAKQHSWEIRTPDINPAWYAGRGIRPVGRF 31

BLOSUM62 Gapop 10.0 . Gapext 0.5 Scoring lable:

127863 seqs. 47025705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : -

Pred. No. :s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMMARIES

			bos tau	P81278 rattus nerv	P81277 homo sapien	•	6											O83527 treponema p	homo sapre						P94972 mycobacteri					٠.	Q57996 methanococc	C9fbm3 streptomyce	P29013 escherichia	_	oryct
SUMMARIES		CI	PERP BOVIN	PRRP_RAT	Parp Human	NER3_BOVIN	NER3 HUMAN	EX71_CORGL	SX71_COREF	UNR_RAT	JVRA METTH	YSB7_FASMU	TVRA_RHILO	JVRA_RHIME	<pre>6PGL_SYNY3</pre>	Y458 XYCPN	SAMB SALTY	UVRA_TREPA	T253 HUMAN	DHI2_RABIT	NER3 RAT	TRBZ METMA	UVRA_VIBCH	UVRA_MYCLE	JVRA_MYCTU	M4K6 MOUSE	ARGC_BACHD	AVP3_ARATH	DAPF_CORGL	Y762 METJA	YS76 METJA		YCGB_ECOL1	=	TGMI_RABIT
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P44410 haemophilus	P57979 pasteurella		P31993 escherichta	P38025 arabidops:s	C9ff80 arabidopsis	Q05013 neisseria r	Q9hqs0 halobacteri	O9jmh7 mus musculu	P39743 saccharomyc	C92935 homo sapien	P22735 homo sapien	
UVRA HAEIN	UVRA_PASMU	TRA2_DROV1	YHHZ ECOLI	PUR7 ARATH	SUVI_ARATH	LIPM NETMB	HISS HALN1	NER3 MOUSE	R167 YEAST	EXER HUMAN	TOME_HUMAN	_
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4 6	46	45.5	45.5	45.5	45.5	45.5	45	45	45	45	45	
34	SE	9	[*·	3.8	33	0	41	42	£ 4	4	45	

ALIGNMENTS

PREDICTION STANDARD; PRE: 98 AA. PRESENCE BOUND PRESENCE BOOK (Rel. 39, Created) 10-MAY-2000 (Rel. 39, Last sequence update) 20-MAY-2000 (Rel. 39, Last sequence update) Prolactin-releasing peptide precursor (PrRF: (Prolactin releasing hormone) (Contains: Prolactin-releasing peptide PrRP20) Prolactin-releasing peptide precursor (PrRF: (Prolactin releasing hormone) (Contains: Prolactin-releasing peptide PrRP20) BOS taurus (Bovine) BOS tautus (Bos tautu	basic residues. PEPTIDE PRRP31. PEPTIDE PRRP20. VIDE AMIDE GROUP).	Length 98; Indels 0; Gaps 0:
BOULN PRRP_BCVIN STANDARD; PRT: 98 AA. 10-RED-2000 (Rel. 39, Created) 10-MAY-2000 (Rel. 39, Last sequence update) 10-MAY-2000 (Rel. 39, Last sequence update) 10-RED-2003 (Rel. 41, Last annotation update) 10-RED-2003 (Rel. 41, Last update) 10-RED-2003 (Rel. 41, Rel. 41,	EMBL; AB015417; BAA29025.1; HORMOLE: Amidation; Signal; Cleavage on pair of basic residues. SIGNAL 1 22 PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP31. PEPTIDE 33 53 PROLACTIN-RELEASING PEPTIDE PRRP31. PROPED 88 98 AMIDATION (G-54 PROVIDE AMIDE GROUP) SEQUENCE 98 AM: 10544 MM: G8AC35A1380FA908 CRC64:	100.0%; Score 172: DB 1; 100.0%; Pred. No. 1.8e-18: ive 0; Mismatches 0;
PERDILL 1 PRRP_BOULN DAY -2000 (Rel. 39, Created) T 30-MAY-2000 (Rel. 39, Last sequence update of the control	EMBL; AB015417; BAA29025.1; BAA29025.1; SIGNAL 1 22 PEPTIDE 23 53 PEPTIDE 33 53 PROPED 88 98 NOD RES 53 53 SEQUENCE 98 AA: 10544 MM	Ouery Match Best Local Similarity 100 Matches 31: Conservative
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P81277;
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Matches
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                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 2).
STRAIN-Sprague-Dawley, TISSUE=Hypothalamus;
Anderson S.T., Kokay I.C., Lang T., Gratian D.R., Curlewis J.D.;
"Quantitation of prolactin-releasing peptide (PPRP) mRNA expression in specific brain regions during the rat oestrous cycle and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMIDATION (G-53 PROVIDE AMIDE GROUP).
TPDINPAMYTGRGIRPVGRFGRRATPRDVTGLGQLSCLPL
DGRTKFSQRG -> SECLTYGRQPLTSFHPFTSQMPP (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PR1. ALTERNATIVE PRODUCTS:
                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota, Metazoa: Chordata: Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                      s:
                              PRRF MAI

281278: QBK3YC;

30-MAY-2000 (Rel. 39, Last sequence update)

30-MAY-2000 (Rel. 41. Last annotation update)

28-FBB-2003 (Rel. 41. Last annotation update)

Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing

Prolactin-releasing peptide PrRP31; Prolactin-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sumino Y., Firino M., Tissue distribution of projectin-releasing peptide (FIRP) and its

    Pept. 83:1-10:1999).
    PUNCTION: Stimulates prolactin (PRL) release and regulates the

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Iso_d=P81278-2; Sequence=VSP 004370;
-!- IISSUE SPECIFICITY: Wide:y expressed, with highest levels in
medulia oblongata and hypothalamus.
                                                                                                                                                                                                                                                      Fukusumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
PROLACTIN-RELEASING PEPTIDE PRRP31.
PROLACTIN-RELEASING PEPTIDE PRRP20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hormone; Amidation; Signal; Cleavage on pair of basic residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY.
MEDLINE=99446652; PubNed=16498338:
Fujil R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hir
Sekiguchi M., Kitada C., Kurokawa T., Nishimura C., Onda H.,
Sumino Y., Fujino M.,
                                                                                                                                                                                                                                    MEDLINE=98268781; PubMed=9607765;
Hinuma S., Habata Y., Fujii R., Kawamata Y., Hoscya M., Fuk
Kitada C., Masuo Y., Asano T., Matsunoto H., Sekiguchi M.,
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactia-releasing peptide in the brain.";
Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Svent=Alternalive splicing: Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P81278-1; Sequence=Displayed:
                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
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                            STANDARD:
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; JC7607; JC7607.
                                                                                                                                                                                    NCBI_TaxID=10116;
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33
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                                                                                                                                                                                                                                                                                                                                                                                                lactation."
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VARSPLIC
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                            PRRF RAT
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PEPTIDE
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RESULT 2
               PRRP RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.
                                                                                                                                                   Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-WAY-2000 (Rel. 39, Last sequence update)
By BerBel-2003 (Rel. 41, Last annordation update)
Prolactin-releasing peptide precursor (PRRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PRRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleosioni.
Mammalia, Eutheria, Primates. Catarinini. Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99426652; PubMed=10498338;
Fujii R., Fukusumi S., Hosoya M., Rawamata Y., Habala Y., Himura ,
Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMIDATION (G-54 PROVIDE AMIDE GROUP)
229A2F3F50CF981B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fukusuma
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PROMACTIN-RELEASING PEPTIDE PRRP20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sumino Y., Fujino M.;
"Tissue distribution of prolactin-releasing peptide (PrRP) and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 158; DB 1; Length 87:
Pred. No. 1.9e-16;
1; Nismatches 2; Indels
                                                                                      Score 163: DB 1: Length 83:
Pred, No. 3.3e-17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., F. Kitada C., Masuo Y., Asano T., Matsumoro H., Sekiguchi M. Kurokawa T., Nishimura O., Onda H., Fujino M., M. Aprolactin-releasing peptide in the brain.";
Nature 393:272-276 (1998).
                                                                                                                                                indels
/FTId=VSP_004370.
DCC75AZ64EEE4F29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  Ž
                                                                                                                                                                                                          1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                                               22 SRAHQHSMETRIPDINPAWYTGRGIRPVGRF 52
                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain:
MEDLINE=98268781; PubMed=9607765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
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90.3%;
                                 9215 NW;
                                                                                            94.8%;
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                                                                                                                       93.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          releasing peptide PrRP20]
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Best Local Similarity 90.3
Matches 28; Conservative
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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                                                                                                                    Local Similarity
es 29; Conserv
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                                 83 AA;
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                                                                                                                                                                    (Gangiloside sialidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning and characterization of a plasma membrane-associated sialidase Specific for gangliosides.";

7. Biol. Chem. 274:5004-5011(1999).

-!- FUNCTION: Plays a role in modulating the ganglioside content of the lipid bilayer at the level of membrane-bound sialyl
                                                                                                                                                                                                                                                                                                                                                                                                                       glycoconjugates.
CATALYTIC ACTIVITY: Hydrolysis of alpha (2->3)-, alpha (2->5)-,
                                                                                                                                                                                                                                                                                                                              ŝ
                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata: Euteleostori,
Mammalia, Eutheria, Cetarticdactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                 TISSUE=Brain:
MEDLINE=99143165; PubMed=9938745;
Miyagi T., Wada T., Iwamatsu A., Hata X., Yosbikawa Y., Tokuyama
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., PARTIAL SECUENCE, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.5%; Score 61; DB 1; Length 428; 40.7%; Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418B34F3245A8F2; CRC64;
                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sialidase 3 (EC 2.2.1.18) (Membrane sialidase)
/N-acetyl-alpha-neuraminidase 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRIP MOTIF.
By similarity.
Potential.
Potential.
           SRAHOMSMEIRTPDINPAWYAGAGIRPVGRE 31
                       23 SRTHRHSMEIRTPOINPAWYASRGIRPVGRF 53
                                                                                                    428 AA
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InterPro; IPRC02860; GH BNR.
Pfan; PF0212; BNR. 3.
Hydrciase; Glycosidase; Membrar
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                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                  Bovidae; Bovinae; Bos.
                                                                                                                                                                                                          Bos taurus (Bovine)
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428 AA;
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Best Local Similarity
Matches 11: Conserv
                                                                                                                                                                                                                                                             NCBI_TaxID=9913;
                                                                                                  NER3 BCVIN
097859;
28-FEB-2003 (
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Gaps

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Indels

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Pred. No. 0.2; 6; Mismatches

Conservalive

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                                                                                                                                                                     NER3_HUMAN STANDARD; PRT; 428 AA.
AC Q9UG49, Q9NQB1.
DT 28-FEB-2003 (Rel. 41, Last sequence update:
DT 28-FEB-2003 (Rel. 41, Last sequence update:
DT 28-FEB-2003 (Rel. 41, Last sequence update:
DT 28-FEB-2003 (Rel. 41, Last sequence update:
DT 28-FEB-2003 (Rel. 41, Last minitare)
DT 28-FEB-2003 (Rel. 41, Last minitare)
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"Cloning, expression, and chromosomal mapping of a human gangiloside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. J. 349:343-35:(2000).
-!- FUNCTION: Plays a role in modulating the ganglioside content of the lipid bilayer at the level of membrane-bound sialyi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venerando
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Verrebrata, Euteleosiomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fundation of Marsey M.T., Papini N., Riboni M., Manzoni M., Venerand Croci G., Preti A., Ballabio A., Tettamanti G., Borsani G., "Identification and expression of NEU3, a novel human sialidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM: 604617; -...
MIM: 604617; -...
GO: GO: 0005887; C: integral to plasma membrane: TAS.
GO: GO: 0006889; Panglioside catabolism; TAS.
InterPro: IPR002860; GH BNR.
Pfam; PFC2012; BNR: 3.
Hydroiase; Glycosidase; Membrane; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 261:21-27(1999).
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FRIP MOTIF.
By similarity.
                                    RAHQHSMEIRTPDINPAWYAGRGIRPV 28
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Biochem. J. 349:343-351 (2000).
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EMBL; Y18563; CAB96131.1; ALT_INIT
Genew; HGNC:7760; NEU3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99335353; PubMed=10405317
                                                                                                                                                                                                                                                                                                                                                                         (N-acetyl-alpha-meuraminidase 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISUE Skeietal muscle;
PubMed=10861246;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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203
244
35
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                                                                                                                                                                                                                                                                                                                                                                                                          "The entire genomic sequence of Gorynebacterium efficiens YS-314."; Submitted (MAY-2002) to the EMBL/Genbank/DDB databases.
-!- FUNCTION: Bidirectionally degrades single-stranded DNA into large acid-insoluble oligonucleotides, which are then degraded further into small acid-soluble oligonucleotides (By similarity).
-:- CATALYTIC ACTIVITY: Exomucleolytic cleavage in either 5' to 3'-cr 3'-to 5'-direction to yield nucleoside 5'-phosphates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae: Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- SUBUNIT: Heterooligomer composed of large and small subunits (By
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
KAWARADAYASI Y., Yamazaki J., Hino Y., Kikuch: H., Nakamura Y.,
Ikeo K., Suzuki M., Mashima J., Ilcoh T., Yamagishi A., Nishio Y.,
                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52; DB 1; Length 447;
Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF_00378; -; 1.
InterPro; IPR003753; Exonuc_VII_L.
Pfam: PFC2601; Exonuc_VII_L; 1.
TIGRFAMS: TIGR00237; XES#; 1.
Hydro.ase; Nuclease; Exonuclease; Complete proteome.
SEQUENÇE 447 Aa; 49051 MW; FDBDF6A768E742C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- SUBCELLUÍAR LOCATION: Cytoplasmic (By similarity).
                                                                       15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last amnoration update)
Probable exodeoxyribonuclease VII large subunit
Exonuclease VII large subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNR_RAT STANDARD, PRT, 798 AA. P18395; 01-NOV-1990 (Rel. 16, Created) 01-NOV-1990 (Rel. 16, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                              44.7 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 PAFYAGRGSFSLWVTDIRPVG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 PAWYAGRG-----IRPVG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMB1; AP005217; BAC17888.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.18;
                                                                                                                                                                                                          Corynebacterium efficiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 57.1
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Usuda Y., Sugimoto S.;
                                                                                                                                                                                                                                                                   NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
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UNR.
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                         EX7L_COREF
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                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBE outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions along as its content is in me way modified and this statement is not removed. Usage by and for commercial
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or send an email to lidense@isb-sib.ch/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SUBUNIT: Heterooligomer composed of large and small subunits '3y similarity'.
-: SUBCEDIULAR LOCATION: Cytoplasmic (By Similarity).
-: SIMILARITY: BELONGS TO THE NSEA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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28-FEB-2003 (Rel. 41, Last seguence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
                                                                                                                                                                                   32.6%; Score 56; DB 2; Length 428; 37.0%; Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 417;
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                                                                                                                                                                                                                             Indels
                                                                                                                        Potential.
: 35D1DD9359A78C98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; Nuclease; Exonuclease; Complete proteome.
SEQUENCE 417 AA; 45582 MW; B32CD9286C173C34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 52: DB 1;
Pred. No. 4.1:
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By similarity.
Potential.
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                       195 KTRPHSLMIYSDDLGVTWHHGRLIRPM 221
                                                                                                                                                                                                                                                                 2 RAHOHSMEIRTPDINPAWYAGRGIRPV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MF 00378; -; 1.
InterPro; IPR033753; Exonuc_VII_L.
Pfam; PF02601; Exonuc_VII_L; 1.
TIGRFAMs; TIGR00237; XseA; :.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAFYAGRGTFSLWVTDIRPVG 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Exonuclease VII large subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP005277; BAB99418.1; -.
                                                                                                                                             48252 MM:
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57.1%;
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Best Local Similarity
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OBNRM3;
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NCBI_TaxID=747;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last Sequence update)
41, Last annotation update)
UNTABC SYSTEM protein A (UVIA protein) (Excinuclease ABC subunit A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAINDELTA H;

MEDLINE=98037514 FubbRed=59371463:
Smith D.R., Doucetre-Stam L.A., Deloughery C., Lee H.-M., Dubois G. Aldredge T., Bashirzacha R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Warg Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Satertoveki J., Gibson R., McDougall S., Shimer G., Goyal A., Pletroveki S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N., "Complete genome sequence of Methanobacterium thermoautotrophicum delitah: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                  Methanobacterium thermoautorrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.7%: Score 51: DB I; Length 798: llarity 43.5%: Pred, No. 12; Conservative 5: Mismatches 8: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5484337A8B0995A4 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSD 1.
CSD 2 (INCOMPLETE).
CSD 3.
CSD 4 (INCOMPLETE).
CSD 6.
CSD 6.
CSD 7.
CSD 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        962 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    583 HSVNGITEEANPTIYSGKVIRPL 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 HSMEIRTPDINPAWYAGRGIRPV 28
                   MEDLINE=90370473: PubMed=2204029
                                                                                                                                                                                                                                                                                                                                            EMBL: X5231: CAA36549.1: -.
PIR: S11210; S11210
MSSP, P1527: 1113C.
InterPro: IPR002059: Cold_shock.
Pfam: PF00313; CSD: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                Prodom, PD000621: Cold shock: 1.
SMART, SM00357; CSP: 5.
PROSITE: PS00352; COLD_SHOCK: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88894 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               674 7
796 A.A.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 10, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE PROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JURA OR MTH443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UVRA METTH
026543:
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This SWISS-PROT entry is copyrigh. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EXBL ourstation. the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions, as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                            (By similarity).
-:- SUBUNIT: Forms a heterotetramer with uvrB during the search for lesions (By similarity).
-:- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-:- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA recombination:
FUNCTION: The UvrABC repair system catalyzes the recognition and processing of DNA lesions. UvPA is an ATPase and a DNA-binding protein. A damage recognition| complex composed of 2 uvrA and 2 uvrB subunits scans DNA for abnormalities. When the presence of lesion has been verified by uyrB, the uvrA molecules dissociate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V., "Complete genomic sequence of Pareuralla multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-: SIMILARITY: BELONGS TO THE FRUCTOSAMINE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
18
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Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                               Score 51: DB 1; Length 962:
Pred. No. 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108395 MW; 2COEF7FC41CCDC60 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; H69157; H69157.

HAWAP: NF 0205; -; I.

HAWAP: NF 0205; -; I.

HIGEPPO: IPR003439; ABC_transporter.

InterPro; IPR004662; JvrR.

InterPro; IPR004662; JvrR.

From: PP00005; ABC_transporter: I.

SMART: SM00382; AAA; 2.

TIGREMMS; TIGR00630; uvra; I.

PROSITE: PS00211; ABC_TRANSPORTER_I; 2.

PROSITE: PS0093; ABC_TRANSPORTER_I; 2.

SOS response: Excision nuclease: DNA repair: DNA republication and excision; ATP-binding; DNA-binding; Repeat; 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 RTPDINPAWYAG ......RGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.7%; Scor. No. 19. 39.5%; Pred. No. 19. 19. 19. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (POTENTIAL)
ATP (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C4-TYPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000828; AAB84949.1; -.
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                             -:- SUBUNIT: Forms a heteroteiramer with uvrB during the search for lessons [Bs similarity).
-!- SUBCESLULAR BOCATION: Cytopiasmic (By similarity).
-!- SUBCESLULAR: BELONGS TO THE ABC TRANSPCRIER FAMILY. UVRA SUBFAMILY.
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                   28-FEE-2003 (Rel. 41, Created)
28-FEE-2003 (Rel. 41, Last sequence update)
28-FEE-2003 (Rel. 41, Last annotation update)
UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lesion has been verified by uvrB, the uvrA molecules dissociate (By similarity).
                                                                                                                                                 ó
                                                                  Interpro, FR05581; Fructosamin kin.
Pfam; PF03881; Fructosamin kin. 1.
Hypothetical protein; Transferase; Kinase; Complete proteome.
SEQUENCE 288 AA: 33778 WM; F4D2F6C26014D940 CRC64;
                                                                                                                                                                                                                                                                                                                     .uvka ok mikujo.
Rhizobiu: loti (Mesorhizobium loti).
Bacteria: Proteobacteria; Alphaproteobacteria: Shizobiales;
PhyllobacTeriaceae; Mesorhizobium.
                                                                                                                       Similarity 37.5%; Pred. No. 5.4; 9; Conservative 6; Mismatches 9; Indels
                                                                                                                                                                                                                                                973 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probom; PD000066; ABC transporter; I. TIGREAMS; TIGR00630; uvra; 1. PROSITE; PS00211; ABC TRANSPORTER 1; 2. PROSITE; PS50893; ABC TRANSPORTER 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP, MP_00205; -; 1.
InterPro: IPR003439; ABC_transporter.
InterPro: IPR004602; UvrĀ.
PF00005; ABC_tran; 2.
                                                                                                                                                                                  5 OHSMEIRTPDINPAWYAGRGIRPV 28
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMB1; AP002995; BAB48277.1; -.
                                                         EMBL; AE006094: AAK02671.1:
                                                                                                                                                                                                                                               STANDARD:
                                                                                                                          Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MAFF303099;
                                                                                                                                                                                                                                                                                                                 CVRA OR MLR0750
                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=381:
                                                                                                                                                                                                                                                UVRA RHILO
098M36;
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-:- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-:- SUBCELLULAR LOCATION: TO THE ABC TRANSPORTER FAMILY. UVRA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *Regalation of divergent transcription from the uvrA-sst promoters in Sincrhizobium melilori.", Mol. Genet. 26:112-130(1999).
Mol. Genet. 26:112-130(1999).
Mol. Genet. 26:112-130(1999).
Processing of DNA lesions. UvrA is an ATPase and a DNA-binding processing of DNA lesions. UvrA is an ATPase and a DNA-binding protein. A damage recognition complex composed of Z uvrA and 2 uvrA motes behavits scans DNA for abnormalities. When the presence of a lesion has been verified by dvrB, the uvrA motecules dissociate
                                                                                                                                                                                                                                                                                                                                     Gaps
   response; Excision nuclease; DNA repair: DNA recombination;
excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDI-NE-2196507; PubMed=11481430; Capela D. Barloy-Hubler F., Gcuzy J., Bothe G., Ampe F., Balur J., Capela D., Barloy-Hubler F., Gcuzy J., Bothe G., Ampe F., Balur S., Boiter A., Boutry M., Cadeu E., Dreamo S., Gloux S., Godra T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger J., Renard C., Thebault P., Vandenboll M., Weidner S., Galibert F., Analysis of the chromosome sequence of the legume symbiont Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
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30-MAY-2000 (Rel. 39, Last sequence update)
38-FBR-2003 (Rel. 41, Last annotation update)
UVABC system protein 4 (UVA protein) (Excinuclease ABC subunit
UVABC SYSTOR SMC01235.
Rhizobium meliloti (Sinorhizobium meliloti)
                                                                                                                                                                                                                                                                                                                                     ..
28
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Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
NCBI_TaxID=382;
                                                                                                                                                                                                                                                                    Leng=h 973:
                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                             C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 716 RIPRSNPATYTGAFIPIRDWFAGLPBAKARGYQP-GRF 752
                                                                                                                                                                                                                                                                                                                                                                                                   11 RTPDINPA-----WYAG-----RGIRPVGRF 31
                                                                                                                                                                                                                                                             Score 50: D8 1:
Pred. No. 19;
                                                                                                ATP (POTENTIAL)
                                                                                                                                     (PCTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  973 AA
                                                                                                                                                                                                                                                                                                                              2; Mismatches
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InterPro; IPR003439; ABC_transpotter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=2021;
MEDLINE=99430868; PubMed=10503543;
                                                                                                                                     ATP
                                                                                                                                                                                                   973 AA; 107358 MW;
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                                                                    Complete proteome
                                                                                                                                                                                                                                                                    29.18:
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                                                                                                                                                                                                                                                                                                                                     Matches I5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                     669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tapias A.. 8arbe J.;
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SOS response; E
DNA excision; R
Zinc-finger; C
NP BIND
NP BIND
SON_FING
761
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Transmembrane; Complete proteome:
                                                                                                                                                                                                                                                                                Y468 MYCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pneumoniae
                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                  Y468_MYCPN
                                                                                                                                                       Matches
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844888788
84888788
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                                                                                                                                                                                                                                                    ۵,
           Pfam; PF00005; ABC_tran; 2.
Probom; PD000006; ABC_transporter; 1.
TIGREMA: TIGRO630. uvra: ...
TIGREMA: TIGRO630. uvra: ...
PROSITE; PS00211; ABC_TRANSPORTER_2; 1.
SOS response; Excision nuclease: DNA repair; DNA recombination: DNA excision, ATP-binding; Exclaing; P-binding; NP-binding; Repeat: Zinc; Metal-binding: NP_binD 34 41
                                                                                                                                                                                                                                                    Gards
Salves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phospho-D-giuconate.
ATHWAY: Sencore phosphate pathway; second step.
SIMILMARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE 6-PHOSPHATE ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaneko I., Sato S., Kocani H., Tahaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Mattaino A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Tamada M., Tabata S.:
"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions:"
DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sazuka T., Chara O.; "Towards a profece of cyanobacterium Synechocystis sp. "Towards a profeome project of cyanobacterium Synechocystis sp. strain PCC6803: linking 130 protein spots with their respective
                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                   29.1%; Score 50: DB 1; Length 972; larity 39.5%; Pred. No. 19; Conservative 2: Mismatches 1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ġ
                                                                                                                                                                                             107191 MW; 3ELABB14527A47FE CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Electrophoresis 18:1252-1258(1997).
-:- FUNCTION: HYDROLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO (
FHOSPHOGLUCONAIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Cyanobacteria; Chroccoccales; Symechocystis
                                                                                                                                                                                                                                                                                                         716 RIPRSNPATYTGAFIPIRDWFAGLPBAKARGYQP-GRF 752
                                                                                                                                                                                                                                                                                11 RIPDINPA-----WYAG-----RGIRPVGRF 31
                                                                                                                       ATP (POTENTIAL).
ATP (POTENTIAL).
C4-TYPE.
G -> MIN REF. 2).
F -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                        01-NCV-1597 (Rel. 35, Created)
01-NVV-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
PGL OR DEVB OR SLL1479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE OF 1-19.
MEDLINE=97443974; PubMed=9298645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97061201; PubMed=8905231;
InterPro: IPR004602; Uvra.
                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                      787
                                                                                                                                                                19
67
973 AA;
                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 15, Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCB1 TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                            6PGL SYNY3
974618;
                                                                                                                                                                CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                    NP_BIND
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                6PGL_SYNY3
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H
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STRAINS=ATCC 29342 / M129;
MEDLINS=66.17562; PubMed=8604303;
Hilbert H., Himmed-reich R., Plagens H., Herrmann R.;
"Sequence analysis of 56 kb from the genome of the bacrerium "Nycoplasma pneumoniae comprising the draA region, the arp operon and cluster of xibosemal protein genes."
Nucleic Acids Res. 24:628-639(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete sequence analysis of the genome of the bacterium Mycopiasma
                                                                                                                                                                                                                                                                                                                                      Gaps
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MEDLINE=21088919; PubMed=11271496;
Regula J.T., Ueberla B., Boguth G., Goerg A., Schnoelzer M.,
Herrmann R., Frank R.,
"Towards a two-dimensional protecome map of Mycopiasma pneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Electrophores:s 21:3765-3780(2000).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-|- SIMILARITY: SOME. TO MG064.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycoplasma pneumoniae.
Bacteria, Firmicutes, Moilicuies, Mycoplasmataceae, Mycoplasma.
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                                                                                                                                                                                                                                                                                 Length 259:
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STRAIN=ATCC 29342 / M129;
MEDLINEATCC 9910555; PubMed=8948633;
Himmelreich R., Hilbert H., Plagens H., Plrkl E., Dl B.-C.
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                   239 AA; 26351 NW; 9C64A0A342325917 CRC64;
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Last annotation update)
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Pred. No. 7.5;
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EMBL, D90916; BAA18726.1; ALT_INIT.
InterPro; IPR006148; Gluc gal isom.
Interpro; IPR005900; Phosphogluconlac.
Pfam: Pf01182; Glucosamine iso; I.
IIGRFAMS; TIGR01198; pgl. I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 24:4420-4449(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein MG468 homolog (K05_orf1882).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION BY MASS SPECTROMETRY
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01-NOV-1997 (Rel. 35; Created)
01-NOV-1997 (Rel. 35; Last seq
28-FEB-2003 (Rel. 41; Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000017; AAB95806.1; -.
                                                                                                                                                              Hydrolase, Complete proteome. INIT MET 0 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003838; DUF214. 
Pfam; PF02687; FtsX: 1.
                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARE;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmoneila typhimurium.
Jasmud Go-mba cryptic.
Bacteria; Proleobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriacese; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmoneila typhimurium has two homologous but different umuDC operons: cloning of a new umuDC-like operon (satAB) present in 60-megadalton cryptic plasmid of S. typhimurium.; J. Bacteriol. 173:1051-1063:1991).
-!- FUNCTION: INVOLVED IN UP PROTECTION AND MUTATION.
-!- SIMILARITY: BELCNGS TO THE DNA POLYMERASE TYPE-Y FAMILY.
-!- SIMILARITY: Contains 1 :muC domain.
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                    1007 POTENTIAL.
1100 POTENTIAL.
11170 POTENTIAL.
11719 POTENTIAL.
11719 POTENTIAL.
11827 POTENTIAL.
11848 POTENTIAL.
11871 POTENTIAL.
1871 POTENTIAL.
1871 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nohmi T., Hakura A., Nakai Y., Watanabe M., Murayama S.Y.,
Sofuni T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB 1; Length 424;
Pred. No. 16;
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                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                        Score 48.5; DB
Pred. No. 64;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                        1 SRAHOHSMEIRTPDINPAWYAGRGIRFVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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PIR: B38176; B38176; B38176; B38176; B10123; atypical; i.
InterPro; IPR001126; UMUC_like.
Pfam; PP00817; IMS; i.
PROSITE; PSS0173; UMUC; l.
PROSITE; PSS0173; UMUC; l.
Plasmid; SOS mutagenesis: DNA repair.
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MEDLINE=91123176; PubMed=1991707;
                                                                                                                                                                                                                                                                   28.2%; Sccilarity 32.3%; Pre
Conservative 5;
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Best Local Similarity
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1080
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11828
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P23832;
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Title: Perfect score:

Scoring table:

Searched:

Segnence:

830525 segs, 258052624 residues BLOSUM62 Gapop 10.5 , Gapext 5.5

830525 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 160% Listing first 45 summaries

Database -

SPTREMBL_23:*

1: Sp_arGhea:*

2: sp_bacteria:*

3: Sp_tung:*

5: Sp_tung:*

6: Sp_ammal:*

7: Sp_morate:*

8: Sp_plant:*

8: Sp_plant:*

9: Sp_plant:*

1: Sp_plant:*

1: Sp_virus:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	OSW112 CVIS BRIES	O9w624 carassius a	O91876 rhodospiril	Ogui£9 homo sapten	095v18 ciona savio	060687 homo sapien	OBww85 homo sapien	OBywc7 anabaena so	Ogipa4 rhodocyclus	O9krvi vibrio chol	OCBERS SACCHARONYC	09rvp2 deinococcus	OBrosamus mascala	Oskifs mus musculu		Q8uc89 agrobacteri
	CI	CEMN12	Q9W624	QFLaJ6	Centre Centre	95YJ8	060687	Q8WW85	Q8YWC7	Q9CPA4	COKRYT	008689	C9RYP2	C8R054	CSKIFB	CSUSIS	68DD80
	En DB	9 86	117 13	692 2	54 4	55 5	465 4	65 4	303 16	36 2	02 16	76 3	76 16	67 11	68 11	73 16	08 16
	Query Match Length DB		.i.	36.0 6			33.1 4				31.7 5		30.8 376			30.2	
*		100.0	63	36	EB	33	33	33	32	32	 	M			30	ကိ	8
	Score	172	104	62	57	57	5.2	57	56.5	55	54.5	53.5	53	53	53	52	52
	Result No.	. 1	7	m	ব	ıΩ	9	7	60	o	10	11	12	13	14	15	16

,	G8ukp2 agrobacteri		COL		นาดน				brass	C912w4 pseudomonas	C8per0 xanthomonas	Q19530 caenorhabdi	urki	C96sd4 homo sapien	CHO:	OBixtz nome sapien	Enm		·O	QBr3r: mus musculu		Q91wSC mus musculu	Q8t4u2 manduca sex	Q8tts7 methancsard	Q887e3 oryza sativ	6]	S		Q8pq42 xanthomonas	
	OSUKPZ	OBCBT2	08F0P1	Q8C720	QBRTV7	Q9ZGE5	09ES77	294KU5	Q94FZ9	2911W4	O8PER 3	019530	087474	Q963D4	08N6Q2	Q8IXT2	08CGM9	C27142	Q9VRV3	Q8R3R1	Q8JZN2	091450	08T4U2	Q8TTS7	C8S7E3	CBZTET	C93.227	Q9M3.7.	Q8PQ42	
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•		440	447	949	13	1292	98	327	327	664	194	294	315	333	367	367	370	450	514	689	767	798	1563	1845	292	374	420	190	217	
•	200	30.2	30.2	30.2	30.2	30.2	О	o,	29.9	29.9		29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.4	29.4	29.4	29.4	29.1	
i	25					25		1	51.5	급.					5.		51	51	51	51	.ı	51	51	21	0	0	50.5	0	20	
	7.7	8,1	6,1	20	21	22	23	24	Z 52	171		B 7	29	30	31	3.5	33	34	25	36	3.7	38	3.9	C 4	41	542	43	44	113 147	

ALIGNMENTS

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8	Q8WN12			•
ΠD	OBWN12 PRELIMINARY;	PRT: 58 AA.	びらず	
Ä				
5	: 01-MAR-2002 (TrEMBLrel: 2	, Created)		
Ë	CI-MAR-2002 (TrEMBLrel 2	, Last sequence update:		
ဌ	1 01-MAR-2002 (TrEMBLrel. 20, Last annotation updat	, Last annotation update)		
ព	Preproprolactin-releasing peptide.	peptide.		
SO	Ovis aries (Sheep).			
S		Sukaryota, Metazoa, Chordata, Cramiata, Vertebrata, Euleleostomi,	Euleleostomi;	
Ö		Mammaila, Sutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,	scora; Bovoidea;	
Ö				
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ö.		_		
n.	SECUENCE PROM N.A.			
Ä		.L., Barclay J.L., Anders	5.3.3	
E : Or;		de (Prar, in the ewe: CD)	A cloning mana	
n:	distribution and effects on prolactin secretion in vitro and in	n prolactin secretion in	vitro and in	
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ις. •Τ		Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.	SAISON.	
S				
SO		SEQUENCE 98 AA; 10513 MW; 2A53331ED62CAABS CRC64;	. 50	
~	Oxery Match	 	. 80	
. ,	Similarity	100.0%; Pred. No. 9.2e-17:		
-	40		Indels 0; Gaps 0;	
6	1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31	AWYAGRGIRPVGRF 31		

23 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 53

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Created)
Last Sequence update)
Last annotation update) 117 A.A. PRT; Q9W624 Q9W624; 01-NOV-1999 (TEMBLE1.12, 01-NOV-1999 (TEMBLE1.12, 01-DEC-2001 (TEMBLE1.19, RESULT 2 Q9W624 ID Q9W6; AC Q9W6; D7 01-NC DT 01-NC

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PRELIMINARY;
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SEQUENCE FROM N.A.
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Matches
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Q95YJ8
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              Carassius auratus (GO:dfish).
Bukaryota, Metazoa: Chordata, Craniara, Vertebrata: Euteleostomi:
Actinopierygii, Meopterygii, Teleostei, Ostariophysi: Cypriniformes,
Cyprinidae: Carassius.
NCBL Tax1D=7957;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DJ47937.3 (Sushi-repeat protein (SRPUL)) (Fragment).
DJ47937.3.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAINES;
MEDLINE=20138142; PubMed=10671438;
Cheng V.S., Brantner C.A., Tsapin A., Collins M.L.P.;
Cheng V.S., Brantner C.A., Tsapin of the photochemical reaction
"Role of the H protein in assembly of the photochemical reaction
center and intracytoplasmic membrane in Rhodospirillum rubrum.";
D. Bacceriol. 182:1200-1207:2002.
EMBL, AF20219; AR37352.1: -
InterPro: IPR003672; CobN/Mg_chitase.
Fram; PP02514; cobN-Mg_chei; I.
NOW TER.
SEQÜENCE 692 AA; 75433 WW: 96430AE938P35680 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria: Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae, Rhodospirillum.
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                                                                                                                                                                                                                                                                                                                                          ch 60.5%; Score 104; DB 13; Length 117; 1 Similarity 57.7%; Pred. No. 4.8e-07; 15; Conservative 8; Mismatches 3; Indels (
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                                                                                                                                                                                                   Satake H., Minakata H., Pujimoto M.;
"Carassius RFamide (C-RF amide) ".
"Carassius RFamide (C-RF amide) ".
Submitted (MOV-1998) to the EMBL/GenBank/JDBJ databases.
EMBL: ABO20024; BAA75662.1; "DSDC4CB22038C2B0 CRC64;
SEQUENCE 117 AA; 12879 FW; DSDC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Brain;
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Phiebobranchia; Cionidae; Ciona.
MCBI_TaxID=51511;
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Mammalia, Eutheria, Primates, Catarrhini. Hominidae. Homo.
NCBI_TaxID=9606;
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Kurosawa H., Inukai T., Inaba T., Goi K., Chang K.-S., Sinjyo T.,
Rakestraw K.M., Naeve C.W., Look T.A.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                         6: Indels
[1]
SECUENCE FROM N.A.
Lawlor 5.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBL databases.
EMBL; AL035608; CAB55682.i; -.
NON TER 54 54
SEQUENCE 54 AA; 6110 NW; E2F3C39F7B961A9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     imal K.S., Satch N., Satcu Y.;
"Clone acvignyl genes.",
"Chone acvignyl genes.",
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB05;747; BAB68156.1; -
InterPro: IPR07097; Znf C2H2.
Pfam: PF00096; zf-C7H2: 4
SWART; SM00355; ZnF C2H2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AJG-1998 (TrEMBLrel. 07, Created)
01-AJG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Sushi-repeat protein (Sushi-repeat containing protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ES8FSDEDD812E8AC CRC64;
                                                                                                                                                                                             Length
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01-DBC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Zic_related protein la.
                                                                                                                                                                                        Score 57; DB 4;
Pred. No. 0.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        355 AA
                                                                                                                                                                                                                                       Vismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
Metal-binding; Zinc; Zinc-finger.
SEQUENCE 355 AA; 40876 MW; E58F5DEDD8
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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18 TPAVTPTWYAGSGYYP 33
                                                                                                                                                                                        33.1%;
56.2%;
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                                                                                                                                                                Query Match
Best Local Similarity 56.2%,
                                                                                                                                                                                                                                                                                     12 TPDINPAWYAGRGIRP
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es 12; Conservative
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23

Gaps

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Length 303:

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A Marabe T., Nakamura Y., Wolk C.F.; Kuritz T., Sasamoto S.,
A Watatabe A., Iriguoti M., Ishikawa A., Kawashma K., Kimura T.,
A Kishida Y., Kohara M., Matsunoto M., Mateuno A., Muraki A.,
A Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada Y.,
A Yasuda M., Tabata S.,
Toyanobacterium Anabaena S.,
Complete genomic sequence of the filamento:s nitrogen.fixing
Cyanobacterium Anabaena Sp. strain PCC 7120.",
L DNA Res. 81-205-213 (2001).
E EMBL, APO03586; BAB78052.1, -
FEMBL, APO03586; BAB78052.1, -
FinterPro: IFR004843; M-ppestrase.
Fram: PFO0149; Metallophos; 1.
W Hyporhetical protein; Complete profecome.
SEQUENCE 303 AA: 34449 MW: 689700B2127EE987 CRC64;
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51.6%; Pred. No. 7:
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                                                   MEDL1NE=21595285, PubMed=11759840;
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Best Local Similarity 51.6'
Matches 16: Conservative
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Ruang C.-H., Chen H.. Peng J., Chen Y.,
"Cloning and characterization of the sushi-repeat containing protein
(SRP) as a novel interaction partner of Rh type C glycoprotein
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Mammaita, Eutheria, Prinates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Bacteria: Cyanobacteria: Nostocales: Nostocaceae; Nostoc.
NCBI_TaxID=103690;
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                                                                                                                                            Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AT060567; AAC15765.1; -.
EMBL: AF393649; AAM73693.1; -.
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Submitted %7AN-2002% to the EMBL/GenBank/DDBJ databases.
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Pfam; PF026494; Sush; 1.
ProstIE: P800006; CYICCHROME P450; 1.
SEQUENCE 465 AA; 52971 NN; 4D7523187FF3EFB6 CRC64;
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EMBL, BCC2073; AAH20733.1; ...
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR001416; Hyalin.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PP00084; Sushi_3.
SMART; SMO032; CCP, 3.
PROSITE; P500086; CYTOCHROME_P450; 1.
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Homo sapiens (Human).
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Photosynthesis:
mechanisms and effects (Proceedings of the lith international congress
on photosynthesis), pp.4:2889-2892, Kluwer Academic Publishers,
Dozdrecht (1999).
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"Primary structure and transcription of genes encoding B870 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=IL144;
MEDLINE=20031519; PubMed=10563807;
Menin L., Yoshida M., Jaquinod M., Nagashima K.V.. Matsuura K.,
Parot P., Vermeglio A.;
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                                                                                                                                                                                                                                Rhodocyclus gelatinosus (Rhodopseudomonas gelatinosa).
Bacteria, Proteobacteria, Betaproteobacteria, Burkhoideriales,
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"Photosynthetic gene cluster in purple bacterium, Rubrivivax
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MEDLINE=94132007; PubMed=8300574;
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Saccharomyces cerevisiae (Baker's yeast).
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SEQUENCE FROM N.A.
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STRAINEEL TOR N16961, Serotype O1;

MEDLINE=2040683; PubMed=10352301;

Heidelberg J.F., Eben G.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Pererson J.D., Umayar L.A.,

Soldin S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragon I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smirh H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

"DNA sequence of both chromosomes of the cholera pathogen Vibrio

cholerae.":
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
  midpoint potential cytochrome oB in the photosynthetic bacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vibrio cholerae.
Bacceria, Proteobacteria, Gammaproteobacteria, Vibrionales,
Vibrionaceae, Vibrio.
VCBI_TaxID=666;
                                                                                                                                                                                                       32.0%; Score 55; DB 2; Length I236;
llarity 34.4%; Pred. No. 49;
Conservative 6; Mismatches 9; Indels
                                                                                                                                                               1236 AA: 134729 NW; 84051C045638520C CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  503 AA; 55997 MW; 2ABD94A2336C9E48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q08689;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Las: sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Chromosome XV reading frame ORF YOR253W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                          1112 SEQVALETRIRMLNPKWYEGMLEHGYEGVÄQI 1143
                                                                                                                                                                                                                                                                                                  3 AHQHSMEIRTPDINPAWYAG-----RGIRPV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 503 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435 SSSASHSVELDTTQAR-EWFMGRDVRPEGQ 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 406.477-483 (2000).

EMBL. AEC34228, AAF94657.1; ...

TIGR. VC1502. ...

InterPro: IPR001678; Sun. Nopi/Nop2.

Pfam. PFC1189; Noli Nop2 Sun; 1.

TIGREPMS: TIGR0046; nop2p; 1.

PROSITE, PSC1153; NOLi NOP2 SUN; 1.

Complete Procecne.

SEQUENCE 501 AA; 55997 NW; 2ABD948
                     Rubrivivax gelatinosus.";
Biochemistry 18:15218-15244(1999).
BMBL: ABG34704: BAA34057.1; -.
InterPro, IPR03572; CobK/Mg_chltase.
Pfam: PF025.4; cobx.Mg_chel: 1.
Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sun/nucieolar protein family protein.
VCISO2.
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Best Local Similarity 36.7
Matches 11, Conservative
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hes 11; Conserv
                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                          Query Maich
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Q08689
ID Q0868
AC Q0868
DT 01-NO
DT 01-NC
DT 01-MA
DE Chrom
GN ARD2
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
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CO
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MEDLINE=20036896; PubMed=10567266; White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Nodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffatt K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Wamarhevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.C., Venter J.C.,
                                                                                                                                                                                                                                                                                              Jaunaux J.C., Poirey R.;

"Sequencing analysis of a 36.9 kb fragment of yeast chromosome XV
"reveals 26 open reading frames including SEC63, CDC31, SUG2. GCD1,
Yeast 12:483-487(1997).

"BEL2, PNT1, PAC1 and VPH1.",
Yeast 12:483-487(1997).

"BEL2, SC5161, CDAA99475.1,
"InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR000182; GCN5acetyltr4nsf.
Sukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes
Saccharomycetales, Saccharomycetaceae, Saccharomyces,
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(1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.8%; Score 53; DB 16; Length 376; 40.0%; Pred, No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deinococcus radiodurans.
Bacteria, Deinococcus-Thermus, Deinococci; Deinococcales:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                  Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4F09DC597A690BAC CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         376 AA; 39845 MW; 7AB7FF32F8C45651 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SRAHQHSMEIRTP---DINPAWYAGRGIRPVG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
31.1%; Score 53.5; DE
Best Local Similarity 31.2%; Pred, No. 11;
Matches 10; Conservative 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; FF00583; Acetyltransf; i.
PROSITE; PS00190; CYTOCHROWE C; 1.
SEQUENCE 176 AA; 19727 MW; 4F9
                                                                                                                                                                                                                                                                           MEDLINE=97298311; PubMed=9153759;
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EMBL: AE001863; AAF12376.1; -
TIGR: DRA0268; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deinococcaceae; Deinococcus.
NCBI_TaxID=1299;
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Search completed: November 12, 2003, 11:09:32 Job time : 37 secs
     PDINPAWYAGRGIRP 27
                                20 PAVTPTWYAGSGYSP 34
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AGR L 109.
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TISSUE=Kidney;

Huang C.-H.. Chen H., Perg J., Chen Y.;

"Clothing and characterization of the sush-repeat containing protein (SRP) as a novel interaction partner of Rh Type C glycoprotein (RRCG).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                      Eukaryota, Metazoa: Chordata: Craniata; Vertebrata: Buteleostom:;
Mammalia: Eutheria: Rodentia; Sciurognathi: Muridae: Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QRKIFB;
QRKIFB;
QUI-0CT-2002 (TEMBLrel. 22, Created;
O1-0CT-2002 (TEMBLrel. 22, Last sequence update)
O1-0CT-2003 (TEMBLrel. 23, Last sequence update)
O1-MAR-2003 (TEMBLrel. 23, Last annotation update)
Sushi-repeat containing protein.
Mus musculus (Mouse).
Bukaryota; Metazoa; Clordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae; Musinae; Mus.
(**)
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O
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Submitted (AFR-2002) to the EMBL/SenBank/DDBJ databases.
EMBL: BGG8107: AAH280107.1.
R MSD: MGI:194.6042: 1110039007Rik.
R InterPro; IFR001128; Cytochrome_P450.
R InterPro; IFR004128; Cytochrome_P450.
R InterPro; IFR004346; Sushi.SCR_CCP.
R Pfcar; PF02094; HYR; I.
Pfam; PF03094; HYR; I.
R SWART; SM00342: CCP. 3.
R R SWART; S000346; CYTOCHROME_P450; I.
R R SWART; SCO0346; CYTOCHROME_P450; I.
                                                                                                                                                                                                                                                                                                                                                                                                 32.8%: Score 53; DB 11: Length 467; 53.3%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-2001) to the EMBL/JenBank/DDBJ databases.
RMGD, AR93840, AAM73691.1;
RMGD, MG1:1916042; 1110039COTRİK.
IncerPro: IPR00128; Cytochrome_P450.
IncerPro: IPR00138; Cytochrome_P450.
InterPro: IPR00138; Sushi_SCR_CCP.
Rfam; PF02494; HYR; 1.
Rfam; PF02494; HYR; 1.
Rfam; PF02084; Sushi; 3.
SMART; SM00032; CCP; 3.
RPOSITE; PS000086; CYTOCH; 3.
SEQUENCE 468 AA: 51180; WF 151A952070DC40D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.8%; Score 53; DB 11; Length 469; 53.3%; Pred. No. 34;
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468 AA: 5318G YM: 151A952070DC40D4 CRC64;
                                                  Ol-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
Similar to sushi-repeat protein.
1110039C07RIK.
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                             467 AA
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                             PHT:
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Best Local Similarity 53.3.
8: Conservative
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                            PRELIMINARY:
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                              SEQUENCE FROM N.A.
                                         28R054:
01-JJN-2002
                            Q8R054
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RESULT 13
Q8R054
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MEDLINE=21608551; PubMed=11743194; Miller N. Blanchard M. Goddner B., Hinkle G., Gattung S., Miller N. Blanchard M. Goddner B., Hinkle G., Gattung S., Miller N. Blanchard M. Goldnen B.S., Gattung S., Miller N., Bakenazi X., Halling C., Xullin D., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A. Liu F. Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A. Liu F. Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A. Liu F. Houmiel K., Gordon J., Lomo C., Eappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Sirub G., Gielo C., Slater S.:
"Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefacters S8.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                              Agrobacterium tumefaciens (strain) (58 / ATCC 33970).
Bacteria, Proteobacteria, Alphaproteobacteria: Enizobiales:
Enizobiaceae, Rhizobium.
NCB: TaxiD=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 30.2%; Score 52; DB 16; Length 73; Best Local Similarity 47.6%; Pred. No. 6.9; Matches 10; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL: AE008203; AAK88619.1; -. SEQUENCE 73 AA; 8219 MW; 02A6F70FA651F2AB CRC64;
                                                                    01-JUN-2002 (TrEMBirel, 21, Created) 01-JUN-2002 (TrEMBirel, 21, Last sequence update) 01-JUN-2002 (TrEMBirel, 21, Last annotation update)
        73 AA
    PRT
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PRELIMINARY:
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